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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:15:56 ; Search time 44 Seconds
(Without alignments)
43.697 Million cell updates/sec

Title: US-09-651-685a-5

Sequence: 1 CCYDASVNNDETCEQRAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	95.6	1676	1 C5HU	complement C5 prec
2	94	82.5	74	2 A25408	complement C5 - bo
3	93	81.6	74	2 A01268	complement C5 - p1
4	84	73.7	77	2 A57689	complement C5a - r
5	84	73.7	1680	1 C5MS	complement C5 prec
6	56.5	49.6	1735	2 S54784	sex-limited protel
7	56.5	49.6	1736	2 A29176	sex-limited protel
8	56.5	49.6	1738	1 A24558	complement C4 prec
9	55.5	48.7	76	2 J10036	complement C4a ana
10	55.5	48.7	77	2 A01265	complement C4 - bo
11	51.5	45.2	1744	1 C4HU	complement C4a pre
12	48	42.1	135	2 D44503	p19 protein - beet
13	48	42.1	282	2 UC5677	RNA4 protein - beet
14	48	42.1	282	2 C44503	P31 protein - beet
15	47	41.2	834	2 J01965	hypothetical 94K p
16	46	40.4	1473	2 A20872	ovostatin precursor
17	45.5	39.9	1617	2 T28153	complement C4 - ch
18	45	39.5	159	2 E86760	conserved hypotet
19	45	39.5	394	2 T21013	hypothetical prote
20	44.5	39.0	161	2 S44619	C50C3.9 protein -
21	44.5	39.0	281	2 S73895	hypothetical prote
22	44.5	39.0	669	2 S65551	factor H - bovine
23	44	38.6	68	2 AE3441	17k common-antigen
24	44	38.6	2095	2 S29529	genome polypeptide
25	43.5	38.2	241	2 A58262	tetraspan TSPAN-1
26	43.5	38.2	1651	1 C3NJ	complement C3 prec
27	43	37.7	198	2 H90111	26S proteasome, be
28	43	37.7	337	2 T18654	hypothetical prote
29	43	37.7	461	2 AH0373	cysteine-tRNA 11ga

30	43	37.7	1645	2 AG1897	two-component hybr
31	43	37.7	2543	2 T31687	surface antigen - p
32	42.5	37.3	685	2 S78040	fibulin, splice fo
33	42.5	37.3	705	2 S34968	fibulin, splice fo
34	42.5	37.3	1620	2 S15339	complement compone
35	42.5	37.3	1673	2 T50806	complement compone
36	42	36.8	368	2 H75412	spermidine/putresc
37	42	36.8	1068	2 S01519	genome polypeptide
38	42	36.8	2092	2 S30026	genome polypeptide
39	42	36.8	2149	2 S18676	hypothetical prote
40	41.5	36.4	312	2 T32379	hypothetical prote
41	41.5	36.4	616	2 T32379	hypothetical prote
42	41.5	36.4	1101	2 T16840	hypothetical prote
43	41	36.0	187	2 T48093	hypothetical prote
44	41	36.0	208	2 C96833	hypothetical prote
45	41	36.0	217	2 A87990	protein W05H12.1 [

ALIGNMENTS

RESULT 1
C5HU
complement C5 precursor [validated] - human
N:Contains: C5a anaphylatoxin; C5b
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text_change 08-Dec-2000
C:Accession: A40075; A27689; A01267; A01266; S15121
R:Hayland, D.L.; Hayland, J.C.; Fleischner, D.T.; Hunt, A.; Wetsel, R.A.
J. Immunol. 146, 362-368, 1991
A:Title: Complete cDNA sequence of human complement pro-C5. Evidence of truncated tra
A:Reference number: A40075; MUID:91079575; PMID:1984448
A:Accession: A40075
A:Molecule type: mRNA
A:Residues: 1-1676 <HAV>
A:Cross-references: GB:M57729; NID:g179982; PIDN:AAA51925.1; PID:g179983
A:Note: S18-Ser was also found
R:Wetsel, R.A.; Lemons, R.S.; Le Beau, M.M.; Barnum, S.R.; Noack, D.; Tack, B.F.
Biochemistry 27, 1474-1482, 1988
A:Title: Molecular analysis of human complement component C5: localization of the str
A:Reference number: A27689; MUID:88209511; PMID:3365401
A:Accession: A27689
A:Molecule type: mRNA
A:Residues: 412-1676 <MET>
A:Cross-references: GB:M65134; GB:M18879; NID:g179691; PIDN:AAA51856.1; PID:g179692
R:Fernandez, H.N.; Hugli, T.E.
J. Biol. Chem. 253, 6955-6964, 1978
A:Title: Primary structural analysis of the polypeptide portion of human C5a anaphyla
A:Reference number: A01267; MUID:79005687; PMID:690134
A:Accession: A01267
A:Molecule type: protein
A:Residues: 678-751 <PER>
R:Lundvall, A.B.; Wetsel, R.A.; Kristensen, T.; Whitehead, A.S.; Woods, D.E.; Ogden,
J. Biol. Chem. 260, 2108-2112, 1985
A:Title: Isolation and sequence analysis of a cDNA clone encoding the fifth complemen
A:Reference number: A01266; MUID:85130937; PMID:2579066
A:Accession: A01266
A:Molecule type: mRNA
A:Residues: 412-854, 'STALSRLCNGKISGCKRLRPGSSDSFASASQVAGITGTHHHAQT' <LUN>
A:Cross-references: GB:K02874
A:Note: The carboxyl-terminal part of the sequence in this report appears to be deriv
R:Bohnsack, J.F.; Mollison, K.W.; Buko, A.M.; Ashworth, J.C.; Hill, H.R.
Biochem. J. 273, 635-640, 1991
A:Title: Group B streptococci inactivate complement component C5a by enzymic cleavage
A:Reference number: S15121; MUID:91144547; PMID:1996561
A:Contents: annotation
C:Comment: Complement C5 contains two disulfide-linked chains, formed by removal of f
(beta and alpha' chains).
C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement
is the foundation upon which the membrane attack complex is assembled.
C:Comment: C5a has potent spasmogenic and chemotactic activity.
A:Gene: GDB:C5

A:Cross-references: GDB:119734; OMIM:120900
 A:Map position: 9q34.1-9q34.1
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; 1
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-673,678-1676/Product: complement C5 #status predicted <NMT>
 F:19-673,752-1676/Product: C5b #status predicted <C5B>
 F:19-673/Product: complement C5 and C5b beta chain #status predicted <C5A>
 F:678-1676/Product: complement C5 alpha chain #status predicted <C5B>
 F:752-1676/Product: C5a anaphylatoxin #status experimental <C5T>
 F:567-673,678-1676,698-724,699-731,711-732,866-1527,1101-1159,1375-1505,1405-1474,1520-15
 F:741/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:751-752/Cleavage site: Arg-Leu (C5 convertase) #status experimental
 F:911,1115,1630/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 95.6%; Score 109; DB 1; Length 1676;
 Best Local Similarity 95.0%; Pred. No. 1.6e-08;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 CCYDGASVNNDETCERAR 20
 Db 698 CCYDGASVNNDETCERAR 717
 ||||| ||||| ||||| |||||

RESULT 2
 A25408
 Complement C5 - bovine (fragment)
 N:Contains: C5a anaphylatoxin; C5b
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 02-Jun-1988 #sequence_revision 15-Oct-1994 #text_change 16-Feb-1997
 C:Accession: A25408
 R:Gennaro, R.; Simonic, T.; Negri, A.; Motola, C.; Secchi, C.; Ronchi, S.; Romeo, D.
 Eur. J. Biochem. 155, 77-86, 1986
 A:Title: C5a fragment of bovine complement. Purification, bioassays, amino-acid sequence
 A:Reference number: A25408; MUID:86136134; PMID:3081348
 A:Accession: A25408
 A:Molecule type: Protein
 A:Residues: 1-74 <GEN>
 C:Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four
 (beta and alpha' chains).
 C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement co
 is the foundation upon which the membrane attack complex is assembled.
 C:Comment: C5a has potent spasmogenic and chemotactic activity.
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; 1
 F:1-74/Product: C5a anaphylatoxin #status experimental <C5T>
 F:21-47,22-54,34-55/Disulfide bonds: #status predicted

Query Match 82.5%; Score 94; DB 2; Length 74;
 Best Local Similarity 80.0%; Pred. No. 1.7e-07;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 CCYDGASVNNDETCERAR 20
 Db 21 CCYDGASVNNDETCERAR 40
 ||||| ||||| ||||| |||||

RESULT 3
 A01268
 Complement C5 - pig (fragment)
 N:Contains: C5a anaphylatoxin; C5b
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 29-Jul-1981 #sequence_revision 15-Oct-1994 #text_change 16-Feb-1997
 C:Accession: A01268; A26248
 R:Gerard, C.; Hugli, T.E.
 J. Biol. Chem. 255, 4710-4715, 1980
 A:Title: Amino acid sequence of the anaphylatoxin from the fifth component of porcine co
 A:Reference number: A01268; MUID:80182137; PMID:7372604
 A:Accession: A01268
 A:Molecule type: protein
 A:Residues: 1-74 <GEN>
 R:Gerard, C.; Hugli, T.E.

Proc. Natl. Acad. Sci. U.S.A. 78, 1833-1837, 1981
 A:Reference number: A26247; MUID:81199549; PMID:6940191
 A:Contents: annotation: active region
 A:Note: although Arg-74 is not essential, residues 72-74 (Leu-Gly-Arg) are required f
 R.Zimmermann, B.; Vogt, W.
 Hoppe-Seyler's Z. Physiol. Chem. 365, 151-158, 1984
 A:Reference number: A26248; MUID:84184201; PMID:6714942
 A:Contents: disulfide bonds
 A:Accession: A26248
 A:Molecule type: protein
 A:Residues: 1-64, 67, 66-73 <ZIM>
 C:Comment: Complement C5 contains two disulfide-linked chains, formed by removal of f
 (beta and alpha' chains).
 C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement
 is the foundation upon which the membrane attack complex is assembled.
 C:Comment: C5a has potent spasmogenic and chemotactic activity.
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein
 F:1-74/Product: C5a anaphylatoxin #status experimental <C5T>
 F:21-47,22-54,34-55/Disulfide bonds: #status experimental

Query Match 81.6%; Score 93; DB 2; Length 74;
 Best Local Similarity 80.0%; Pred. No. 2.4e-07;
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 CCYDGASVNNDETCERAR 20
 Db 21 CCYDGASVNNDETCERAR 40
 ||||| ||||| ||||| |||||

RESULT 4
 A57689
 Complement C5a - rat (fragment)
 N:Contains: C5a anaphylatoxin; C5b
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 23-Feb-1996 #sequence_revision 31-Jan-1997 #text_change 16-Feb-1997
 C:Accession: A57689
 R:Cui, L.; Carney, D.F.; Hugli, T.E.
 Protein Sci. 3, 1169-1177, 1994
 A:Title: Primary structure and functional characterization of rat C5a: an anaphylatox
 A:Reference number: A57689; MUID:95078724; PMID:7987212
 A:Accession: A57689
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 1-77 <CU>
 C:Complex: Complement C5 contains two disulfide-linked chains, formed by removal of f
 (beta and alpha' chains).
 C:Function:
 A:Description: activation of C5 initiates spontaneous assembly of the late complement
 is the foundation for assembly of the membrane attack complex
 A:Pathway: complement alternate pathway; complement pathway
 A:Note: C5a has potent spasmogenic and chemotactic activity
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein
 F:1-77/Product: C5a anaphylatoxin #status experimental <C5T>
 F:24-50,25-57,37-58/Disulfide bonds: #status predicted

Query Match 73.7%; Score 84; DB 2; Length 77;
 Best Local Similarity 75.0%; Pred. No. 6.1e-06;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 CCYDGASVNNDETCERAR 20
 Db 24 CCYDGASVNNDETCERAR 43
 ||||| ||||| ||||| |||||

RESULT 5
 C3MS
 Complement C5 precursor - mouse
 N:Contains: C5a anaphylatoxin; C5b
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Nov-1988 #sequence_revision 15-Oct-1994 #text_change 18-Jun-1999
 C:Accession: A35530; A27538; A40429

R:Wetzel, R.A.; Fleischer, D.T.; Haviland, D.L.
 J. Biol. Chem. 265, 2435-2440, 1990
 A:Title: Deficiency of the murine fifth complement component (C5). A 2-base pair gene deletion.
 A:Reference number: A35530; MUID:90153853; PMID:2303408
 A:Accession: A35530
 A:Molecule type: mRNA
 A:Residues: 1-215 'L' <MET>
 A:Cross-references: GB:M5556; GB:J05234; NID:g192302; PIDN:AAA37348.1; PID:g309123
 R:Wetzel, R.A.; Ogata, R.T.; Tack, B.F.
 Biochemistry 26, 737-743, 1987
 A:Title: Primary structure of the fifth component of murine complement.
 A:Reference number: A27538; MUID:87185363; PMID:2436653
 A:Accession: A27538
 A:Molecule type: mRNA
 A:Residues: 'PGL', 44-1680 <MET2>
 R:Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Wetzel, R.A.
 J. Biol. Chem. 266, 11818-11825, 1991
 A:Title: Structure of the murine fifth complement component (C5) gene. A large, highly intact component gene.
 A:Reference number: A40429; MUID:91268053; PMID:1711041
 A:Accession: A40429
 A:Molecule type: DNA
 A:Residues: 1-15 <HAV>
 A:Cross-references: GB:M64852
 C:Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four (beta and alpha chains).
 C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement cascade, the foundation upon which the membrane attack complex is assembled.
 C:Comment: C5a has potent spasmogenic and chemotactic activity.
 C:Genetics:
 A:Map position: 2
 A:Introns: 22/3; 86/3; 140/3; 164/3; 195/2; 223/1; 253/2; 291/3; 334/1; 372/3; 434/3; 503; 1224/1; 1392/3; 1343/3; 1364/3; 1392/1; 1411/2; 1445/3; 1470/3; 1506/1; 1534/1; 1564/3
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; I
 F:1-18/Domain: signal sequence #status predicted <STG>
 F:19-674, 679-1679/Product: complement C5 #status predicted <C5B>
 F:19-674, 756-1679/Product: complement C5 #status predicted <C5B>
 F:19-674, 756-1679/Product: complement C5 #status predicted <C5B>
 F:679-1679/Product: complement C5 alpha chain #status predicted <C5A>
 F:679-1679/Product: C5a anaphylatoxin #status predicted <C5A>
 F:756-1679/Product: C5b alpha chain #status predicted <C5BA>
 F:567-814, 635-670, 702-728, 703-735, 715-736, 870-1531, 1105-1163, 1379-1509, 1403-1478, 1524-1591, 915, 1119, 1633/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.7%; Score 84; DB 1; Length 1680;
 Best Local Similarity 75.0%; Pred. No. 0.00011;
 Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCYGCASVNDTCGEQRAAR 20
 ||||| || ||||| ||
 Db 702 CCYGCASVNDTCGEQRAAR 721

RESULT 6
 S54784
 sex-limited protein Slp(w7) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
 C:Accession: S54784; MUID:148770
 R:Ogata, R.T.; Zepf, N.E.
 J. Immunol. 147, 2756-2763, 1991
 A:Title: The murine Slp gene. Additional evidence that sex-limited protein has no biologic function.
 A:Reference number: S54784; MUID:92013090; PMID:1918990
 A:Accession: S54784
 A:Molecule type: DNA
 A:Status: preliminary; translation not shown
 A:Residues: 1-1735 <OGA>
 A:Cross-references: EMBL:M64933; NID:g200988; PIDN:AAA40117.1; PID:g200989
 R:Hemmenway, C.; Kaliff, M.; Stavenhagen, J.; Walshall, D.; Robins, D.
 Nucleic Acids Res. 14, 2539-2554, 1986
 A:Title: Sequence comparison of alleles of the fourth component of complement (C4) and S

A:Accession: 148770
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 634-641, 'L', 643-828 <RES>
 A:Cross-references: EMBL:X06455; NID:g54102; PIDN:CAA29761.1; PID:g899336
 C:Genetics:
 A:Introns: 22/2; 86/3; 154/1; 177/3; 207/2; 235/1; 267/2; 302/3; 347/1; 385/3; 444/3; 3; 1219/1; 1296/3; 1352/3; 1372/3; 1404/1; 1464/2; 1494/3; 1519/3; 1554/1; 1584/1; 16
 C:Superfamily: alpha-2-macroglobulin

Query Match 49.6%; Score 56.5; DB 2; Length 1735;
 Best Local Similarity 57.1%; Pred. No. 2;
 Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY 1 CCYDCASVNDTCGEQRAAR 20
 ||||| || ||||| ||
 Db 700 CCYDCASVNDTCGEQRAAR 720

RESULT 7
 A29176
 sex-limited protein precursor - mouse
 M:Alternate names: complement component C4-related sex-limited protein
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
 C:Accession: A29176; B21692; A41195; B29059; B60227; I79467
 R:Ogata, R.T.; Sepich, D.S.
 J. Immunol. 135, 4239-4244, 1985
 A:Title: Murine sex-limited protein: complete cDNA sequence and comparison with murin
 A:Reference number: A29176; MUID:8660918; PMID:3840826
 A:Accession: A29176
 A:Molecule type: mRNA
 A:Residues: 1-1736 <OGA>
 R:Nonaka, M.; Takahashi, M.; Natsume-Sakai, S.; Nonaka, M.; Tanaka, S.; Shimizu, A.;
 Proc. Natl. Acad. Sci. U.S.A. 81, 6822-6826, 1984
 A:Title: Isolation of cDNA clones specifying the fourth component of mouse complement
 A:Reference number: A94013; MUID:85038607; PMID:6208559
 A:Accession: B21692
 A:Molecule type: mRNA
 A:Residues: 651-749, 'H', 751-774, 'D', 776-802, 921-1040 <NON>
 R:Ogata, R.T.; Sepich, D.S.
 Proc. Natl. Acad. Sci. U.S.A. 81, 4908-4911, 1984
 A:Title: Genes for murine fourth complement component (C4) and sex-limited protein (S
 A:Reference number: A41195; MUID:84272739; PMID:6589636
 A:Accession: A41195
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1345-1438, 'R', 1440-1544 <OG2>
 A:Cross-references: GB:K02293; NID:g199611; PIDN:AAA39682.1; PID:g199612
 R:Tosi, M.; Levi-Strauss, M.; Duponchel, C.; Meo, T.
 Philos. Trans. R. Soc. Lond. 306, 389-394, 1984
 A:Title: Sequence heterogeneity of murine complementary DNA clones related to the C4
 A:Reference number: A93753
 A:Accession: B29059
 A:Molecule type: mRNA
 A:Residues: 1255-1335, 'G', 1337-1373 <TOS>
 R:Ogata, R.T.; Zepf, N.E.
 Eur. J. Immunol. 20, 1607-1610, 1990
 A:Title: C4 from C4-high and C4-low mouse strains have identical sequences in the reg
 A:Reference number: A60227; MUID:90353398; PMID:2387317
 A:Accession: B60227
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1096-1139 <OG3>
 A:Cross-references: GB:X55495
 R:Nonaka, M.; Kimura, H.; Teul, Y.D.; Yokoyama, S.; Nakayama, K.; Takahashi, M.
 Proc. Natl. Acad. Sci. U.S.A. 83, 7883-7887, 1986
 A:Title: Identification of the 5'-flanking regulatory region responsible for the diff
 A:Reference number: I59084; MUID:87017050; PMID:3464002
 A:Accession: I79467
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-21 <RES>

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-673/Product: complement C4 beta chain #status predicted <BET>
F:20-673/54-1440,1448-1738/Product: complement C4b #status predicted <C4b>
F:678-1440/Product: complement C4 alpha chain #status predicted <ALP>
F:678-753/Product: C4a anaphylatoxin #status predicted <C4a>
F:754-443/Region: C4b-binding protein binding
F:953-1333/Product: C4d fragment #status predicted <C4d>
F:1448-1738/Product: complement C4 gamma chain #status predicted <GAM>
F:224/743,1387/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:753-754/Cleavage site: Arg-Asn (complement subcomponent C1s) #status predicted
F:1006-1009/Cross-link: thiolester (Cys-Gln) #status predicted

Query Match 49.6%; Score 56.5; DB 1; Length 1738;
Best Local Similarity 57.1%; Pred. No. 2;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDG-ASVNNDETCEQRAR 20
Db 700 CCODGMRKLPKRTCEQRAR 720

RESULT 9

JL0036
complement C4a anaphylatoxin - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 15-Nov-1996
C:Accession: JL0036
R:Cul, L.; Ferreri, K.; Hugli, T.E.
Mol. Immunol. 25, 663-671, 1988
A:Title: Structural characterization of the C4a anaphylatoxin from rat.
A:Reference number: JL0036; MUID:88334568; PMID:3262196
A:Accession: JL0036

A:Molecule type: protein
A:Residues: 1-76 <CU1>
C:Superfamily: alpha-2-macroglobulin
C:Keywords: complement classical pathway; glycoprotein
F:66/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 48.7%; Score 55.5; DB 2; Length 76;
Best Local Similarity 57.1%; Pred. No. 0.15;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDG-ASVNNDETCEQRAR 20
Db 23 CCODGMRKLPKRTCEQRAR 43

RESULT 10

A01265
complement C4 - bovine (fragment)
N:Contains: C4a anaphylatoxin; classical-complement-pathway C3/C5 convertase (EC 3.4.21.1)
C:Species: Bos primigenius taurus (cattle)
C:Date: 13-Jun-1983 #sequence_revision 15-Oct-1994 #text_change 16-Feb-1997
C:Accession: A01265
R:Smith, M.A.; Gerrie, L.M.; Dunbar, B.; Fothergill, J.E.
Biochem. J. 207, 253-260, 1982
A:Title: Primary structure of bovine complement activation fragment C4a, the third anaphylatoxin
A:Reference number: A01265; MUID:83126436; PMID:6760852
A:Accession: A01265
A:Molecule type: protein
A:Residues: 1-77 <SM1>
C:Superfamily: alpha-2-macroglobulin
C:Keywords: complement pathway; glycoprotein; hydrolase; inflammation; plasma; serine protease
F:1-77/Product: C4a anaphylatoxin #status experimental <C4a>

Query Match 48.7%; Score 55.5; DB 2; Length 77;
Best Local Similarity 57.1%; Pred. No. 0.15;
Matches 12; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

OY 1 CCYDG-ASVNNDETCEQRAR 20
Db 23 CCODGMRKLPKRTCEQRAR 43

RESULT 11
C4HU
complement C4a precursor [validated] - human

N:Contains: classical-complement-pathway C3/C5 convertase (EC 3.4.21.43) C4b subunit;
C:Species: Homo sapiens (man)
C:Date: 25-Feb-1985 #sequence_revision 23-Aug-1996 #text_change 08-Dec-2000
C:Accession: I56095; A29177; B29177; A90845; A19311; A92337; S12866; A17265; A32335;
R:Yu, C.Y.
J. Immunol. 146, 1057-1066, 1991

A:Title: The complete exon-intron structure of a human complement component C4a gene.
A:Reference number: I56095; MUID:91108039; PMID:1988494
A:Accession: I56095

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1744 <RES>

A:Cross-references: GB:M59815; NID:g179672; PIDN:AAA51855.1; PID:g179674
R:Belt, K.T.; Yu, C.Y.; Carroll, M.C.; Porter, R.R.
Immunogenetics 21, 173-180, 1985

A:Title: Polymorphism of human complement component C4.
A:Reference number: A29177; MUID:85156269; PMID:3838531
A:Accession: A29177

A:Molecule type: DNA
A:Residues: 1-22 <BEL>

A:Cross-references: GB:M14823
A:Accession: B29177

A:Molecule type: DNA
A:Residues: 1056-1225 <BE3>

A:Cross-references: GB:M14824; NID:g179675; PIDN:AAA52292.1; PID:g553210
R:Belt, K.T.; Carroll, M.C.; Porter, R.R.
Cell 36, 907-914, 1984

A:Title: The structural basis of the multiple forms of human complement component C4.
A:Reference number: A90845; MUID:84155544; PMID:6546707
A:Accession: A90845

A:Molecule type: mRNA
A:Residues: 20-346, 'S', 348-417, 'A', 419-725, 'P', 727-1200, 'S', 1202-1285, 'S', 1287-1418, 1

A:Cross-references: GB:R02403
R:Carroll, M.C.; Porter, R.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 264-267, 1983

A:Title: Cloning of a human complement component C4 gene.
A:Reference number: A19311; MUID:83117835; PMID:6572000
A:Accession: A19311

A:Molecule type: mRNA
A:Residues: 1195-1285, 'S', 1287-1294 <CAR>

A:Cross-references: GB:J00080; NID:g30010; PIDN:CAA23760.1; PID:g1335030
R:Moore, K.E.; Gorski, J.P.; Hugli, T.E.
J. Biol. Chem. 256, 8685-8692, 1981

A:Title: Complete primary structure of human C4a anaphylatoxin.
A:Reference number: A92337; MUID:81264286; PMID:6167582
A:Accession: A92337

A:Molecule type: protein
A:Residues: 680-725, 'PN', 728-756 <MOO>

A:Cross-references: GB:R02403
R:Hessing, M.; van't Veer, C.; Hackeng, T.M.; Bouma, B.N.; Iwanaga, S.
FEBS Lett. 271, 131-136, 1990

A:Title: Importance of the alpha(3)-fragment of complement C4 for the binding with C4
A:Reference number: S12866; MUID:91032049; PMID:1699796
A:Accession: S12866

A:Molecule type: protein
A:Residues: 757, 'X', 759-771, 980-990 <HES>

A:Cross-references: GB:R02403
R:Campbell, R.D.; Gagnon, J.; Porter, R.R.
Biochem. J. 199, 359-370, 1981

A:Title: Amino acid sequence around the thiol and reactive acyl groups of human compl
A:Reference number: A17265; MUID:82182029; PMID:6978711
A:Accession: A17265

A:Molecule type: protein
A:Residues: 957-1012, 'E', 1014-1108, 'I', 1110-1175, 'S', 1177-1270, 'V', 1272-1336 <CHA>

A:Cross-references: GB:R02403
R:Chakravarti, D.N.; Campbell, R.D.; Porter, R.R.
Mol. Immunol. 24, 1187-1197, 1987

A:Title: The chemical structure of the C4d fragment of the human complement component
A:Reference number: A32335; MUID:88094444; PMID:3696167
A:Accession: A32335

A:Molecule type: protein
A:Residues: 957-1012, 'E', 1014-1108, 'I', 1110-1175, 'S', 1177-1270, 'V', 1272-1336 <CHA>

A:Cross-references: GB:R02403
R:Chakravarti, D.N.; Campbell, R.D.; Porter, R.R.
Mol. Immunol. 24, 1187-1197, 1987

A:Title: The chemical structure of the C4d fragment of the human complement component
A:Reference number: A32335; MUID:88094444; PMID:3696167
A:Accession: A32335

C:Accession: J01965
R:Takahashi, M.; Toriyama, S.; Hamamatsu, C.; Ishihama, A.
J. Gen. Virol. 74, 769-773, 1993
A:Title: Nucleotide sequence and possible ambisense coding strategy of rice stripe virus
A:Reference number: J01964, MUID:93224901, PMID:8468559
A:Accession: J01965
A:Molecule type: genomic RNA
A:Residues: 1-834 <TRK>
A:Cross-references: DDBJ:DJ1176; NID:9536885; PIDN:BAA02470.1; PID:91199491
C:Superfamily: rice stripe virus hypothetical 94K protein

Query Match 41.2%; Score 47; DB 2; Length 834;
Best Local Similarity 69.2%; Pred. No. 29;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 CYDGASYNDETC 14
||:|||||
Db 69 CYNRASVNFETC 81

Search completed: May 1, 2003, 22:20:06
Job time : 46 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:09:31 : Search time 11 Seconds
(without alignments)
75.412 Million cell updates/sec

Title: US-09-651-685a-5
Perfect score: 114
Sequence: 1 CCYDGSVNNDETCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	95.6	1676	1 CO5_HUMAN	P01031 homo sapien
2	94	82.5	74	1 CO5A_BOVIN	P12082 bos taurus
3	93	81.6	74	1 CO5A_PIG	P01032 sus scrofa
4	84	73.7	76	1 CO5A_RAT	P08650 ratius norv
5	84	73.7	1680	1 CO5_MOUSE	P06684 mus musculu
6	56.5	49.6	1738	1 CO4_MOUSE	P01029 mus musculu
7	55.5	48.7	76	1 CO4A_RAT	P08649 ratius norv
8	55.5	48.7	920	1 CO4_BOVIN	P01030 bos taurus
9	51.5	45.2	1744	1 CO4_HUMAN	P01028 homo sapien
10	48	42.1	282	1 Y32K_BNYG	P19231 beet necrot
11	46	40.4	1473	1 OVOS_CHICK	P20740 gallus gall
12	44.5	39.0	281	1 Y125_MYCPN	P75511 mycoplasma
13	44.5	39.0	685	1 CFAN_BOVIN	Q28085 bos taurus
14	44.5	39.0	1205	1 YLJ9_CAEEL	Q24373 caenorhabdi
15	44	38.6	715	1 S141_HUMAN	Q92503 homo sapien
16	44	38.6	2095	1 RRP1_TOSV	P27800 toscana vir
17	43.5	38.2	1651	1 CO3_NAJNA	Q01833 najia najia
18	43	37.7	337	1 DN12_CAEEL	Q17433 caenorhabdi
19	43	37.7	461	1 SYC_YERPE	Q82c6c yersinia pe
20	42.5	37.3	705	1 FB11_MOUSE	Q08879 mus musculu
21	42.5	37.3	1640	1 CO3_ONCMY	P88093 oncorhynch
22	42.5	37.3	1673	1 CO3_LAMJA	Q00665 lampetra ja
23	42	36.8	241	1 TSNI_HUMAN	Q06633 homo sapien
24	42	36.8	261	1 RFA4_HUMAN	Q13156 homo sapien
25	42	36.8	760	1 AD25_MOUSE	Q91159 mus musculu
26	42	36.8	1068	1 YCF0_MARPO	P12221 marchantia
27	42	36.8	2149	1 RRP1_RVPVZ	P27316 rift valley
28	41.5	36.4	65	1 MT_PARLI	P80367 paracentrol
29	41.5	36.4	486	1 MTR3_HUMAN	P18523 homo sapien
30	41	36.0	332	1 KC2A_MAIZE	P28523 zea mays (m
31	41	36.0	450	1 VD10_BPTU	P11107 bacterioph
32	41	36.0	491	1 Y084_MCTU	Q53209 mycobacteri
33	41	36.0	1826	1 SUI5_RABIT	P07766 oryctolagus

34	41	36.0	2230	1 G0G4_HUMAN	Q13439 homo sapien
35	41	36.0	4543	1 LRP1_CHICK	P98157 gallus gall
36	41	36.0	4660	1 LRP2_RAT	P98158 ratius norv
37	40	35.1	351	1 Y4VJ_RHISN	Q53218 rhizobium s
38	40	35.1	366	1 YGDE_ECOLI	P32066 escherichia
39	40	35.1	448	1 EXG1_YEAST	P23776 saccharomyc
40	40	35.1	448	1 GRAN_DROME	P39572 drosophila
41	40	35.1	538	1 ADEC_MERTH	Q26952 methanobact
42	40	35.1	581	1 PRIM_ECOLI	P02923 escherichia
43	40	35.1	581	1 PRIM_SALTY	P07362 salmonella
44	40	35.1	593	1 PRIM_HAEIN	Q08346 haemophilus
45	40	35.1	813	1 AD33_HUMAN	Q9b211 homo sapien

ALIGNMENTS

RESULT 1
ID CO5_HUMAN STANDARD: PRT: 1676 AA.
AC P01031;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C5 precursor [contains: C5a anaphylatoxin].
CN C5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Haviland D.L., Haviland J.C., Fleischer D.T., Hunt A., Wetzel R.A.;
RT truncated cDNA sequence of human complement pro-C5. Evidence of
RL J. Immunol. 146:362-368(1991).
RN [2]
RP SEQUENCE OF 412-1676 FROM N.A.
RA Wetzel R.A., Lemons R.S., Lebeau M.M., Barnum S.R., Noack D.,
RA Tack B.F.;
RT "Molecular analysis of human complement component C5: localization of
RL Biochemistry 27:1474-1482(1988).
RN [3]
RP SEQUENCE OF 412-902 FROM N.A.
RA MEDLINE=65130937; PubMed=2579066;
RA Lundwall A.B., Wetzel R.A., Kristensen T., Whitehead A.S.,
RA Woods D.E., Ogden R.C., Colten H.R., Tack B.F.;
RT "Isolation and sequence analysis of a cDNA clone encoding the fifth
RL J. Biol. Chem. 260:2108-2112(1985).
RN [4]
RP SEQUENCE OF 678-751.
RA MEDLINE=79005687; PubMed=690134;
RA Fernandez H.N., Hugli T.E.;
RT "Primary structural analysis of the polypeptide portion of human C5a
anaphylatoxin. Polypeptide sequence determination and assignment of
RT the oligosaccharide attachment site in C5a.";
RL J. Biol. Chem. 253:6955-6964(1978).
RN [5]
RP SEQUENCE OF 678-751 FROM N.A.
RA MEDLINE=91144547; PubMed=1996961;
RA Bohnsack J.F., Mollison K.W., Buko A.M., Ashworth J.C., Hill H.R.;
RT "Group B streptococcal inactivate complement component C5a by enzymic
cleavage at the C-terminus.";
RL Biochem. J. 273:635-640(1991).
RN [6]
RP STRUCTURE BY NMR OF C5A.
RA MEDLINE=88309754; PubMed=3408713;
RA Zuidweg E.R.P., Mollison K.W., Henkin J., Carter G.W.;
RT "Sequence-specific assignments in the 1H NMR spectrum of the human

RT inflammatory protein C5a.";
 RN Biochemistry 27:3568-3580(1988).
 [7]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE-89207527; PubMed-2784981;
 RA Zuideweg E.R.P., Nettesheim D.G., Mollison K.W., Carter G.W.;
 RT "tertiary structure of human complement component C5a in solution
 from nuclear magnetic resonance data.";
 RL Biochemistry 28:172-185(1989).
 [8]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE-89274164; PubMed-2730871;
 RA Zuideweg E.R.P., Fesik S.W.;
 RT "Heteronuclear three-dimensional NMR spectroscopy of the inflammatory
 protein C5a.";
 RL Biochemistry 28:2387-2391(1989).
 [9]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE-97160477; PubMed-9007977;
 RA Zhang X., Boyar W., Galakatos N., Gonnella N.C.;
 RT "Solution structure of a unique C5a semi-synthetic antagonist:
 implications in receptor binding.";
 RL Protein Sci. 6:65-72(1997).
 [10]
 RP STRUCTURE BY NMR OF C5A.
 RX MEDLINE-97332508; PubMed-9188742;
 RA Zhang X., Boyar W., Toth M.J., Mennog L., Gonnella N.C.;
 RT "Structural definition of the C5a C terminus by two-dimensional
 nuclear magnetic resonance spectroscopy.";
 RL Proteins 28:261-267(1997).
 [11]
 CC -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE
 SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS. C5-C9,
 INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE
 FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYTC
 COMPLEX IS ASSEMBLED.
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
 POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
 MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
 CC -1- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC
 RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
 BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN,
 RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA
 CHAIN).
 CC -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
 ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL: M57729; AAA51925.1; -;
 DR EMBL: M65134; AAA51836.1; -;
 DR PIR: A40075; CSHU.
 DR PIR: S15121; S15121.
 DR PDB: 1KJS; 15-MAY-97.
 DR PDB: 1CPA; 17-SEP-97.
 DR Gene: HGNC:1331; C5.
 DR MIM: 120900; -;
 DR InterPro: IPR0002890; AZM_N.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacroglobinA2.
 DR InterPro: IPR001134; Netrin_C.

DR Pfam: PF00207; AZM; 1.
 DR Pfam: PF01759; NTR; 1.
 DR Pfam: PF01821; ANATO; 1.
 DR Pfam: PF01835; AZM_N; 1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR Prodom: PD003264; Anaphylatoxin; 1.
 DR SMART: SM00104; ANATO; 1.
 DR Prosite: PS00477; ALPHA.2.MACROGLOBULIN; FALSE-NEG.
 DR Prosite: PS01177; ANAPHYLATOXIN_2; 1.
 DR Prosite: PS01178; ANAPHYLATOXIN_1; 1.
 KW Complement pathway; Complement alternate pathway; Glycoprotein;
 KW Plasma; Membrane attack complex; Cytolysis; Inflammatory response;
 KW Signal; Polymorphism; 3D-structure.
 FT SIGNAL 1 18
 FT CHAIN 19 673 POTENTIAL.
 FT PROPEP 674 677 COMPLEMENT C5 BETA CHAIN.
 FT CHAIN 678 1676 COMPLEMENT C5 ALPHA CHAIN.
 FT PEPTIDE 678 751 C5A ANAPHYLATOXIN.
 FT CHAIN 752 1676 C5B (ALPHA').
 FT DOMAIN 698 732 ANAPHYLATOXIN-LIKE.
 FT DISULFID 698 724
 FT DISULFID 699 731
 FT DISULFID 711 732
 FT CARBOHYD 741 741
 FT CARBOHYD 911 911
 FT CARBOHYD 1115 1115
 FT CARBOHYD 1630 1630
 FT VARIANT 518 518
 FT
 SQ SEQUENCE 1676 AA; 188331 MM; 87DCA65FF977D19 CRC64;
 Query Match 1676 AA; 95.6%; Score 109; DB 1; Length 1676;
 Best Local Similarity 95.0%; Pred. No. 3.5e-09;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 698 CCYDGA5VNDEFCEQRAAR 20
 1 CCYDGA5VNDEFCEQRAAR 20
 ||||| ||||| |||||
 ID COSA_BOVIN STANDARD: PRT: 74 AA.
 AC P12082;
 DT 01-OCT-1989 (Rel. 12; Created)
 DT 01-OCT-1989 (Rel. 12; Last sequence update)
 DT 01-FEB-1996 (Rel. 33; Last annotation update)
 DE Complement C5a anaphylatoxin.
 GN C5.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-86136134; PubMed-1081348;
 RA Gennaro R., Simonic T., Negri A., Mottola C., Secchi C., Ronchi S.,
 RA Romeo D.;
 RT "C5a fragment of bovine complement. Purification, bioassays,
 RT amino-acid sequence and other structural studies.";
 RL Eur. J. Biochem. 155:77-86(1986).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE-89005703; PubMed-3262536;
 RA Zarbock J., Gennaro R., Romeo D., Clore G.M., Gronenborn A.M.;
 RT "A proton nuclear magnetic resonance study of the conformation of
 RT bovine anaphylatoxin C5a in solution.";
 RL FEBS Lett. 238:289-294(1988).
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
 CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND

CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
DR PIR: A25408; A25408.
DR HSSP: P01033; 1C5A.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR001840; Anaphylatoxin.
DR InterPro: IPR001599; MacroglobulinA2.
DR Pfam: PF01821; ANATO; 1.
DR PRINTS: PR00004; ANAPHYLATOXN.
DR PRODOM: PD003264; Anaphylatoxin; 1.
DR SMART: SM00104; ANATO; 1.
DR PROSITE: PS00477; ALPHA_2-MACROGLOBULIN; PARTIAL.
DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway: Complement alternate pathway; Plasma;
KW Inflammatory response.
KM DOMAIN 21 55 ANAPHYLATOXIN-LIKE.
FT DISULFID 21 47 BY SIMILARITY.
FT DISULFID 22 54 BY SIMILARITY.
FT DISULFID 34 55 BY SIMILARITY.
SQ SEQUENCE 74 AA; 8517 MW; C09DF742D12D70F6 CRC64;
Query Match 82.5%; Score 94; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 3.3e-08;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCYDASVNDTCERAR 20
DB 21 CCYDGAHRNDETCERAR 40
RESULT 3
COSA_PIG STANDARD; PRT; 74 AA.
ID COSA_PIG
AC P01032;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Complement C5a anaphylatoxin.
GN C5.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=80182137; PubMed=7372604;
RA Gerard C., Hugli T.E.;
RT "Amino acid sequence of the anaphylatoxin from the fifth component of
RT porcine complement.";
RL J. Biol. Chem. 255:4710-4715(1980).
RN [2]
RP ACTIVE REGION.
RX MEDLINE=81199549; PubMed=6940191;
RA Gerard C., Hugli T.E.;
RT "Identification of classical anaphylatoxin as the des-Arg form of the
RT C5a molecule: evidence of a modulator role for the oligosaccharide
RT unit in human des-Arg74-C5a.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:1833-1837(1981).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=90248365; PubMed=2337573;
RA Williamson M.P., Madison V.S.;
RT "Three-dimensional structure of porcine C5adesArg from 1H nuclear
RT magnetic resonance data.";
RL Biochemistry 29:2895-2905(1990).
-1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF

CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
DR PIR: A01268; C5PGAT.
DR PDB: 1C5A; 15-OCT-91.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR001840; Anaphylatoxin.
DR InterPro: IPR001599; MacroglobulinA2.
DR Pfam: PF01821; ANATO; 1.
DR PRINTS: PR00004; ANAPHYLATOXN.
DR PRODOM: PD003264; Anaphylatoxin; 1.
DR SMART: SM00104; ANATO; 1.
DR PROSITE: PS00477; ALPHA_2-MACROGLOBULIN; PARTIAL.
DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway: Complement alternate pathway; Plasma;
KW Inflammatory response; 3d-structure.
KM DOMAIN 21 55 ANAPHYLATOXIN-LIKE.
FT DISULFID 21 47
FT DISULFID 22 54
FT DISULFID 34 55
FT SITE 72 74
FT HELIX 2 11
FT TURN 13 14
FT HELIX 16 26
FT HELIX 34 40
FT HELIX 45 62
FT TURN 63 64
SQ SEQUENCE 74 AA; 8609 MW; 11AAFE294A026EB3 CRC64;
Query Match 81.6%; Score 93; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 4.8e-08;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 CCYDASVNDTCERAR 20
DB 21 CCYDGAHRNDETCERAR 40
RESULT 4
COSA_RAT STANDARD; PRT; 76 AA.
ID COSA_RAT
AC P08650;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Complement C5a anaphylatoxin.
GN C5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RA Cui L.-X., Ferreri K., Hugli T.E.;
RT "Characterization of rat C5a, a uniquely active spasmogen.";
RL Complement 2:18-19(1985).
-1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5,
CC C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
CC BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF
CC POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR
CC MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
DR HSSP: P01031; 1KJS.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR001840; Anaphylatoxin.
DR InterPro: IPR001599; MacroglobulinA2.
DR Pfam: PF01821; ANATO; 1.
DR PRINTS: PR00004; ANAPHYLATOXN.
DR PRODOM: PD003264; Anaphylatoxin; 1.


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DR SMART: SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; PARTIAL.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Complement alternate pathway; Glycoprotein;
KW Plasma; Inflammatory response.
FT DOMAIN 24 58 ANAPHYLATOXIN-LIKE.
FT DISULFID 24 50 BY SIMILARITY.
FT DISULFID 25 57 BY SIMILARITY.
FT DISULFID 37 58 BY SIMILARITY.
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .);
SQ SEQUENCE 76 AA; 8869 MW; 2EC15183A6E54769 CRC64;

Query Match 73.7%; Score 84; DB 1; Length 76;
Best Local Similarity 75.0%; Pred. No. 1.3e-06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 CCYDGAENVNDECEQRAAR 20
DB 24 CCYDGAENVNDECEQRAAR 43
||||| 1 ||||| 1

RESULT 5
CO5_MOUSE STANDARD; PRT; 1680 AA.
AC P0684;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C5 precursor (Hemolytic complement) [Contains: C5A anaphylatoxin].
GN C5 OR HC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90153853; PubMed=2303408;
RA Wetsel R.A., Fleischer D.T., Haviland D.L.;
RT "Deficiency of the murine fifth complement component (C5). A 2-base pair gene deletion in a 5'-exon."
RT J. Biol. Chem. 265:2433-2440(1990).
RN [2]
RP SEQUENCE OF 41-1680 FROM N.A.
RX MEDLINE=87185363; PubMed=2436653;
RA Wetsel R.A., Ogata R.T., Tack B.F.;
RT "Primary structure of the fifth component of murine complement."
RT Biochemistry 26:737-743(1987).
RN [3]
RP -1- FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9, INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYTIC COMPLEX IS ASSEMBLED.
CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C5, C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
CC -1- SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA. LINKED BY A DISULFIDE BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN, RELEASING C5A ANAPHYLATOXIN & GENERATING C5B (BETA CHAIN + ALPHA CHAIN).
CC -1- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
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CC -----
DR EMBL; M35525; AAA37349.1; -.
DR EMBL; M35526; AAA37348.1; -.
DR PIR; A27538; A27538.
DR PIR; A35530; A35530.
DR HSSP; P01031; 1KJS.
DR MGD; MGI:96031; HC.
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxin.
DR InterPro; IPR001599; Macrogloblna2.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01759; NTR; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01835; A2M_N; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR PRODOM; PD003264; ANAPHYLATOXIN_1.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; FALSE_NEG.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Complement alternate pathway; Glycoprotein;
KW Plasma; Membrane attack complex; Cytolysis; Inflammatory response;
KW Signal.
FT SIGNAL 1 18
FT CHAIN 19 1680 COMPLEMENT C5.
FT CHAIN 19 674 COMPLEMENT C5 BETA CHAIN.
FT PROPEP 675 678 COMPLEMENT C5.
FT CHAIN 679 1680 COMPLEMENT C5 ALPHA CHAIN.
FT PEPTIDE 679 755 C5A ANAPHYLATOXIN.
FT CHAIN 756 1680 C5B (ALPHA).
FT DOMAIN 702 736 ANAPHYLATOXIN-LIKE.
FT DISULFID 702 728 BY SIMILARITY.
FT DISULFID 715 736 BY SIMILARITY.
FT CARBOHYD 427 427 BY SIMILARITY.
FT CARBOHYD 915 915 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1119 1119 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1633 1633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 216 216 Y -> L (IN DEFECTIVE VARIANT C5D).
FT VARIANT 217 1680 MISSING (IN DEFECTIVE VARIANT C5D).
SQ SEQUENCE 1680 AA; 188877 MW; 81B55A16FAC7D95C CRC64;

Query Match 73.7%; Score 84; DB 1; Length 1680;
Best Local Similarity 75.0%; Pred. No. 3e-05;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCYDGAENVNDECEQRAAR 20
DB 702 CCYDGAENVNDECEQRAAR 721
||||| 1 ||||| 1

RESULT 6
CO4_MOUSE STANDARD; PRT; 1738 AA.
AC P01029; Q61859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Complement C4 precursor [Contains: C4a anaphylatoxin].
GN C4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85298264; PubMed=3862104;
RA Sepich D.S., Noonan D.J., Ogata R.T.;

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FT DOMAIN 700 734 ANAPHYLATOXIN-LIKE.
 FT DISULFID 700 726 BY SIMILARITY.
 FT DISULFID 701 733 BY SIMILARITY.
 FT DISULFID 714 734 BY SIMILARITY.
 FT THIOLEST 1006 1009 BY SIMILARITY.
 FT MOD_RES 1413 1413 SULFATION.
 FT MOD_RES 1416 1416 SULFATION.
 FT MOD_RES 1417 1417 SULFATION.
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 743 743 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1387 1387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 132 132 F -> Y (IN REF. 4).
 FT CONFLICT 327 327 G -> E (IN REF. 4).
 FT CONFLICT 570 570 O -> E (IN REF. 4).
 FT CONFLICT 720 720 R -> G (IN REF. 5).
 FT CONFLICT 739 740 DL -> AI (IN REF. 5).
 FT CONFLICT 838 838 P -> R (IN REF. 4).
 FT CONFLICT 993 993 P -> L (IN REF. 5).
 FT CONFLICT 1043 1043 D -> E (IN REF. 5).
 FT CONFLICT 1119 1119 V -> A (IN REF. 7).
 FT CONFLICT 1190 1190 K -> T (IN REF. 7).
 FT CONFLICT 1324 1324 A -> S (IN REF. 9).
 FT CONFLICT 1401 1401 G -> N (IN REF. 4).
 FT CONFLICT 1442 1442 R -> K (IN REF. 4).
 FT CONFLICT 1453 1453 A -> V (IN REF. 4).
 SQ SEQUENCE 1738 AA; 192870 MW; D1EE02AE7AB42BFF CRC64;

Query Match Best Local Similarity 49.68; Score 56.5; DB 1; Length 1738;
 Matches 12; Conservative 57.18; Pred. No. 0.67; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDG-ASVNNDETCRORAR 20
 || || : |||||
 Db 700 CCODGWTXLPKMRTCRORAR 720

RESULT 7
 CO4_RAT STANDARD; PRT; 76 AA.
 AC P08649;

DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Complement C4a anaphylatoxin.
 GN C4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP MEDLINE=8834568; PubMed=3262196;
 RA Cui L.-X., Ferreri K., Hugli T.E.;
 RT "Structural characterization of the C4a anaphylatoxin from rat.";
 RL Mol. Immunol. 25:663-671(1988).
 RN [2]

RA Cui L.-X., Ferreri K., Hugli T.E.;
 RT "Characterization of rat anaphylatoxins C4a and C5a.";
 RL Fed. Proc. 44:991-991(1985).
 CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4,
 C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES.

CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
 DR HSP; P01036; J00036.
 DR HSP; P01031; IJ03.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacroglobulinA2.
 DR Pfam: PF01821; ANATO; 1.
 DR PRINTS; PRO0004; ANAPHYLATOXN.

DR ProDom: PD003264; Anaphylatoxin; 1.
 DR SMART; SM00104; ANATO; 1.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN, PARTIAL.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 KW Complement pathway; Plasma; Inflammatory response; Glycoprotein.
 FT DOMAIN 23 57 ANAPHYLATOXIN-LIKE.
 FT DISULFID 23 49 BY SIMILARITY.
 FT DISULFID 24 56 BY SIMILARITY.
 FT DISULFID 37 57 BY SIMILARITY.
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .).
 FT CONFLICT 29 29 T -> A (IN REF. 2).
 SQ SEQUENCE 76 AA; 8594 MW; 96700DB7AFB7C6DB CRC64;

Query Match Best Local Similarity 48.78; Score 55.5; DB 1; Length 76;
 Matches 12; Conservative 57.18; Pred. No. 0.039; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDG-ASVNNDETCRORAR 20
 || || : |||||
 Db 23 CCODGWTXLPKMRTCRORAR 43

RESULT 8
 CO4_BOVIN STANDARD; PRT; 920 AA.
 AC P01030; Q27993; Q27992;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Complement C4 precursor [Contains: C4a anaphylatoxin] (Fragments).
 GN C4.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;

RN [1]
 RP MEDLINE=83126436; PubMed=6760852;
 RA Smith M.A., Gerlie L.M., Dunbar B., Fothergill J.E.;
 RT "Primary structure of bovine complement activation fragment C4a, the
 RT third anaphylatoxin. Purification and complete amino acid sequence.";
 RL Biochem. J. 207:253-260(1982).
 RN [2]
 RP SEQUENCE OF 78-920 FROM N.A.
 RC TISSUE=Liver;

RA Groth D.M.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
 CC CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCESSED BY
 CC ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
 CC ANAPHYLATOXIN.

CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C4,
 C4A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
 CC INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
 CC PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
 CC BASOPHILIC LEUKOCYTES.

CC -1- SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR
 AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER
 CC OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA).
 CC MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY COMPLEX CLASS-III
 CC PROTEIN.

CC -1- SIMILARITY: TO C3, C5 AND ALPHA-2-MACROGLOBULIN.
 CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.

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 CC or send an email to license@isb-sib.ch).

CC EMBL: U16750; AA52751.1; -;
DR EMBL: U16749; AA52750.1; -;
DR PIR: A01265; C4BOAT.
DR HSSP: P01031; 1CFA.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR001840; Anaphylatoxin.
DR InterPro: IPR001599; MacroglobinA2.
DR InterPro: IPR001134; Netrin_C.
DR PRINTS: PR00004; ANAPHYLATOXN.
DR ProDom: PD003264; Anaphylatoxin; 1.
DR SMART: SM00104; ANATO; 1.
DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Plasma; Glycoprotein; Sulfation;
KW Inflammatory response.
FT NON_TER 1 1
FT NON_CONS 77 78
FT CHAIN 342 343
FT PROPEP 623 629
FT CHAIN 630 920
FT PEPTIDE 1 77
FT DOMAIN 23 57
FT DISULFID 23 49
FT DISULFID 24 56
FT THIOLEST 37 57
FT MOD_RES 191 194
FT MOD_RES 593 593
FT MOD_RES 596 596
FT MOD_RES 598 598
FT CARBOHYD 504 504
FT CARBOHYD 567 567
SQ SEQUENCE 920 AA; 101881 MW; 1425A0BD945F5497 CRC64;

Query Match 48.7%; Score 55.5; DB 1; Length 920;
Best Local Similarity 57.1%; Pred. No. 0.5;
Matches 12; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 CCYDGS-VNNDTCBORAR 20
DB 23 CCQDGLRLPMARTEQRAAR 43

RESULT 9
CO4_HUMAN STANDARD; PRT: 1744 AA.
AC P01028; Q9UIP5; Q9NPK5; Q13906; Q13160; Q14835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Complement C4 precursor [Contains: C4a anaphylatoxin].
GN C4A AND C4B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RN [1] SEQUENCE FROM N.A. (C4A AND C4B).
RP TISSUE=Liver;
RX MEDLINE=84156544; PubMed=6546707;
RA Belt K.T., Carroll M.C., Porter R.R.;
RT "The structural basis of the multiple forms of human complement component C4.";
RL Cell 36:907-914(1984).
RN [2]
RN [2] SEQUENCE FROM N.A. (C4A).
RP MEDLINE=91108039; PubMed=1988494;
RA Yu C.Y.;
RT "The complete exon-intron structure of a human complement component C4a gene. DNA sequences, polymorphism, and linkage to the 21-hydroxylase gene.";
RT 21-hydroxylase gene.";

RL J. Immunol. 146:1057-1066(1991).
RN [3]
RN [3] SEQUENCE FROM N.A. (C4B).
RP TISSUE=Blood;
RC MEDLINE=96165032; PubMed=8575831;
RX Ugitali D., Townsend D.C., Christiansen F.T., Dawkins R.L.,
RA Abraham L.J.;
RT "Complete sequence of the complement C4 gene from the HLA-A1, B8,
RT C4A0. C4B1, DR3 haplotype."
RL Immunogenetics 43:250-252(1996).
RN [4]
RN [4] SEQUENCE FROM N.A. (C4B).
RP Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
RA Banta A., Swartzell S., Smith T.M., Spies T., Hood L.;
RT "Sequence determination of 300 kilobases of the human class III MHC
RT locus";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RN [5] SEQUENCE FROM N.A. (C4A).
RP Barlow K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN [6] SEQUENCE OF 1-22 AND 1056-1225 FROM N.A.
RX MEDLINE=85156269; PubMed=383531;
RA Belt K.T., Yu C.Y., Carroll M.C., Porter R.R.;
RT "Polymorphism of human complement component C4.";
RN Immunogenetics 21:173-180(1985).
RN [7]
RN [7] SEQUENCE OF 680-756.
RX MEDLINE=81264286; PubMed=6167582;
RA Moon K.E., Gorski J.P., Hugl T.E.;
RT "Complete primary structure of human C4a anaphylatoxin.";
RL J. Biol. Chem. 256:8685-8692(1981).
RN [8]
RN [8] SEQUENCE OF 957-1044.
RX MEDLINE=82182029; PubMed=6978711;
RA Campbell R.D., Gagnon J., Porter R.R.;
RT "Amino acid sequence around the thiol and reactive acyl groups of
RT human complement component C4.";
RL Biochem. J. 199:359-370(1981).
RN [9]
RN [9] SEQUENCE OF 990-1037.
RX MEDLINE=82150875; PubMed=6950384;
RA Harrison R.A., Thomas M.L., Tack B.F.;
RT "Sequence determination of the thiolester site of the fourth
RT component of human complement.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7388-7392(1981).
RN [10]
RN [10] SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94282044; PubMed=8012361;
RA Sargent C.A., Anderson M.J., Hsieh S.L., Kendall E.,
RA Gomez-Escobar N., Campbell R.D.;
RT "Characterisation of the novel gene G11 lying adjacent to the
RT complement C4a gene in the human major histocompatibility complex.";
RL Hum. Mol. Genet. 3:481-488(1994).
RN [11]
RN [11] SEQUENCE OF 1405-1431, AND SULFATION.
RX MEDLINE=8611851; PubMed=3944109;
RA Hortin G., Sims H., Strauss A.W.;
RT "Identification of the site of sulfation of the fourth component of
RT human complement.";
RL J. Biol. Chem. 261:1786-1793(1986).
RN [12]
RN [12] STRUCTURAL BASIS OF POLYMORPHISM.
RX MEDLINE=87080272; PubMed=2431902;
RA Yu C.Y., Belt K.T., Giles C.M., Campbell R.D., Porter R.R.;
RT "Structural basis of the polymorphism of human complement components
RT C4A and C4B: gene size, polymorphism and antigenicity.";
RL EMBO J. 5:2873-2881(1986).
RN [13]
RN [13] VARIANT C4A6 ALLOTYPES.
RX MEDLINE=92242905; PubMed=1573268;
RA Anderson M.J., Milner C.M., Cotton G.H., Campbell R.D.;

DR	PROSITE; PS01178; ANAPHYLATOXIN.2; 1.		
KM	Complement pathway; Plasma; Glycoprotein; Sulfation; Signal;		
KW	Inflammatory response; Polymorphism; Disease mutation;		
	Blood group antigen.		
FT	SIGNAL	1	19
FT	CHAIN	20	675
FT	PROPEP	676	679
FT	CHAIN	680	1446
FT	PROPEP	1447	1453
FT	CHAIN	1454	1744
FT	PEPTIDE	680	756
FT	DOMAIN	702	736
FT	DISULFID	702	728
FT	DISULFID	703	735
FT	DISULFID	716	736
FT	THIOLEST	1010	1013
FT	MOD_RES	1417	1417
FT	MOD_RES	1420	1420
FT	MOD_RES	1422	1422
FT	CARBOHYD	226	226
FT	CARBOHYD	862	862
FT	CARBOHYD	1328	1328
FT	CARBOHYD	1391	1391
FT	VARIANT	477	477
FT	VARIANT	726	726
FT	VARIANT	726	726
FT	VARIANT	1073	1073
FT	VARIANT	1073	1073

```

QY      1 CCYDGA8-VNNDETGORAR 20          45.2%; Score 51.5; DB 1; Length 1744;
       ||||| : |||||||
DB      702 CCGDYTRLPMRSCORAR 722         Pred. No. 4.1;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

RESULT 10
V32K_BNYVG STANDARD: PRT; 282 AA.
ID V32K_BNYVG
AC P19231;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE RNA-4 hypothetical 31.9 Kda protein.
OS Beet necrotic yellow vein mosaic virus (isolate GI).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyivirus.
OX NCBI Taxid=12257;
RN [1]
RP SEQUENCE FROM N.A.
RA Bouzouba S., Guille H., Jonard G., Richards K., Putz C.;
RT "Nucleotide sequence analysis of RNA-3 and RNA-4 of beet necrotic
RT yellow vein virus, isolates F2 and GI."
RL J. Gen. Virol. 66:1553-1564(1985).
CC -----
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CC -----
DR EMBL: M36897; AAA42800.1; -
DR PIR: C44503; C44503.
DR Hypothetical protein.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 31869 MW; AA7C0351C54FE0CC CRC64;

Query Match 42.1%; Score 48; DB 1; Length 282;
Best Local Similarity 57.1%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

OY 2 CYDASVNDDETC 15
 DB 115 CYSQVSLDELCE 128

RESULT 11
 OYOS_CHICK STANDARD: PRT: 1473 AA.

AC P20740;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Oostatin precursor (Ovomacroglobulin).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oviduct;
 RX MEDLINE=95218210; PubMed=7535598;
 RA Nielsen K.L., Soltrop-Jensen L., Nagase H., Thøgersen H.C.,
 RT Exzerodt M.;
 RT "Amino acid sequence of hen ovomacroglobulin (ovostatin) deduced from
 RT cloned cDNA.";
 RL DNA Seq. 5:111-119(1994).
 RN 12;
 RP SEQUENCE OF 37-49.
 RC TISSUE=Egg white;
 RX MEDLINE=83238315; PubMed=6408074;
 RA Nagase H., Harris E.D. Jr., Woessner J.F., Brew K.;
 RT "Ovostatin: a novel proteinase inhibitor from chicken egg white. I.
 RT Purification, physicochemical properties, and tissue distribution of
 RT ovostatin.";
 RL J. Biol. Chem. 258:7481-7489(1983).
 RN 13;
 RP SEQUENCE OF 976-1028.
 RC TISSUE=Egg white;
 RX MEDLINE=93192299; PubMed=7680577;
 RA Nielsen K.L., Soltrop-Jensen L.;
 RT "Evidence from sequence analysis that hen egg-white ovomacroglobulin
 RT (ovostatin) is devoid of an internal beta-Cys-gamma-Glu thiol
 RT ester.";
 RL Biochim. Biophys. Acta 1162:230-232(1993).
 CC -1- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A
 CC UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH,
 CC CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
 CC FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT
 CC REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH
 CC TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST
 CC LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR
 CC WEIGHT SUBSTRATES IS GREATLY REDUCED).
 CC -1- SUBUNIT: HOMOTETRAMER, WHICH CONSISTS OF TWO PAIRS OF DISULFIDE-
 CC LINKED CHAINS.
 CC -1- PTM: THIS PROTEIN LACKS THE THIOESTER BOND FOUND IN OTHER MEMBERS
 CC OF THIS FAMILY.
 CC -1- PTM: CONTAINS 56 MOL. GLUCOSAMINE PER MOL. SUBUNIT.
 CC -1- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X78801; CAA55384.1; -
 CC EMBL: X78801; CAA55385.1; ALT_INIT.
 CC PIR: A20872; A20872.
 CC HSP: P01023; IBV8.

DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR001599; Macrogloblna2.
 DR Pfam: PF00207; A2M; 1.
 DR Pfam: PF01835; A2M_N; 1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; FALSE_NEG.
 KW Serine protease inhibitor; Glycoprotein; Bait region; Signal.
 FT SIGNAL 1 36
 FT CHAIN 37 1473
 FT CARBOHYD 67 67 OVOSTATIN.
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 342 342 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 588 588 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 757 757 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1141 1141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1221 1221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1315 1315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1347 1347 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 46 46 M -> V (IN REF. 2).
 SO SEQUENCE 1473 AA; 166354 MW; A3306847A1179BF CRC64;

Query Match 40.4%; Score 46; DB 1; Length 1473;
 Best Local Similarity 53.3%; Pred. No. 25;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 6 ASVNDDETCQRRAR 20
 DB 883 AETNDDEACEEALR 897

RESULT 12
 Y125_MYCPN STANDARD: PRT: 281 AA.

ID Y125_MYCPN
 AC P75511;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MG125 homolog (A65_orf281).
 GN MP264 OR MP569.
 OS Mycoplasma pneumoniae.
 CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 ON NCBI_TaxID=2104;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelfreisch R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (E.COLI) / YCSE/YXEH
 CC (B.SUBTILIS) FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE000056; AAB96217.1; -
 DR InterPro: IPR001454; Hlygase/hygrlase.
 DR InterPro: IPR000150; Hypothet_cof.
 DR Pfam: PF00702; Hydrolase; 1.
 DR PROSITE: PS01228; COF-1; 1.
 DR PROSITE: PS01229; COF-2; 1.
 DR Hypothetical protein: Complete proteome.
 KW SEQUENCE 281 AA; 32614 MW; BF44564E7C7FBF11 CRC64;

DISULFID , 219 245

C

EMBT: L1A433: AA227071 3. -----

PIR; S44619; S44619.

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:15:16 ; Search time 84 Seconds

(without alignments)
49.059 Million cell updates/sec

Title: US-09-651-685a-5

Sequence: 1 CCGDASVNNDETCEORAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP-archaea:*
- 2: SP-bacteria:*
- 3: SP-fungi:*
- 4: SP-human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP-phage:*
- 10: SP-plant:*
- 11: SP-rodent:*
- 12: SP-virus:*
- 13: SP-vertebrate:*
- 14: SP_unclassified:*
- 15: SP_rv1rus:*
- 16: SP_bacteriap:*
- 17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	84	73.7	77	11	063078
2	56.5	49.6	1148	11	061372
3	56.5	49.6	1738	11	070346
4	51	44.7	608	5	09V174
5	50.5	44.3	1614	13	098977
6	49.5	43.4	548	5	09M497
7	48	42.1	135	12	085686
8	48	42.1	282	12	09DGS5
9	48	42.1	282	12	09DGS4
10	48	42.1	282	12	09DGS5
11	48	42.1	282	12	09DGS5
12	48	42.1	282	12	09DGS5
13	48	42.1	282	12	09DGS5
14	47.5	41.7	282	12	065670
15	47	41.2	227	5	09DGV9
16	47	41.2	834	12	085429

17	47	41.2	834	12	085430	085430 rice stripe
18	47	41.2	1625	12	055597	055597 garlic viru
19	46	40.4	265	16	08XHS4	08XHS4 clostridium
20	45.5	39.9	1159	13	09YIA6	09YIA6 cyprinus ca
21	45.5	39.9	1640	13	09YIA8	09YIA8 cyprinus ca
22	45.5	39.9	1642	13	09YIB0	09YIB0 cyprinus ca
23	45.5	39.9	1642	13	09YIB0	09YIB0 cyprinus ca
24	45	39.5	159	16	09CGI1	09CGI1 lactococcus
25	45	39.5	163	12	09J813	09J813 spodoptera
26	45	39.5	221	5	09NL25	09NL25 plasmodium
27	45	39.5	226	5	09N6J1	09N6J1 plasmodium
28	45	39.5	226	5	09N6G5	09N6G5 plasmodium
29	45	39.5	226	5	09NL21	09NL21 plasmodium
30	45	39.5	226	5	09G556	09G556 plasmodium
31	45	39.5	226	5	09N681	09N681 plasmodium
32	45	39.5	231	5	09N673	09N673 plasmodium
33	45	39.5	231	5	09NL24	09NL24 plasmodium
34	45	39.5	231	5	09NL23	09NL23 plasmodium
35	45	39.5	231	5	09NL22	09NL22 plasmodium
36	45	39.5	231	5	09NL20	09NL20 plasmodium
37	45	39.5	231	5	09NL19	09NL19 plasmodium
38	45	39.5	236	5	09NL18	09NL18 plasmodium
39	45	39.5	282	12	09DS77	09DS77 beet necrot
40	45	39.5	394	5	093521	093521 caenorhabdi
41	45	39.5	739	2	087381	087381 haemophilus
42	44.5	39.0	1589	13	091588	091588 xenopus lae
43	44.5	39.0	1700	13	091933	091933 cyprinus ca
44	44	38.6	68	16	08YTK5	08YTK5 bruceella me
45	44	38.6	285	12	092015	092015 garlic viru

ALIGNMENTS

RESULT 1	ID	063078	PREDIMINARY:	PRT:	77 AA.
AC	063078;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)				
DE	Cca complement component protein (Fragment).				
GN	Csa.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-LEWIS; TISSUE=LIVER;				
RX	MEDLINE-97236424; PubMed-9116048;				
RA	Rothermel E., Rolf O., Goetze O., Zwilner J.;				
RT	"Nucleotide and corrected amino acid sequence of the functional				
RT	recombinant rat anaphylatoxin Csa."				
RL	Biochim. Biophys. Acta 1351:9-12(1997).				
DR	EMBL; X91892; CAA62994.1; -				
DR	HSSP; P01031; IKJS.				
DR	InterPro: IPR000020; Anaphylatoxin.				
DR	InterPro: IPR001840; Anaphylatoxin.				
DR	Pfam; PF01821; ANATO.1.				
DR	PRINTS; PR00004; ANAPHYLATOXN.				
DR	ProDom; PD003264; Anaphylatoxin.1.				
DR	SMART; SM01177; ANAPHYLATOXIN_1.				
DR	PROSITE; PS01178; ANAPHYLATOXIN_2; 1.				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE	77 AA: 8981 MW; 14141F41CC38BD28 CRC64;			
Query Match		73.7%;	Score 84;	DB 11;	Length 77;
Best Local Similarity		75.0%;	Pred. No. 1.2e-06;		
Matches	15;	Conservative	0;	Mismatches	5;
				Indels	0;
				Gaps	0;

OY 1 CCYDGSVNNDETCEORAR 20
 DB 24 CCYDGSVNNDETCEORAR 43

RESULT 2

ID 061372 PRELIMINARY: PRT: 1148 AA.

AC 061372;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

GN C4 complement protein (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RC STRAIN-B10.D2(C4(H)SLP(A));

RA MEDLINE=86176748; PubMed=3008092;

RA Hemenway C., Kalif M., Stavenhagen J., Walthall D., Robins D.;

RT "Sequence comparison of alleles of the fourth component of complement

(C4) and sex-limited protein (SLP).";

RL Nucleic Acids Res. 14:2539-2554(1986).

DR EMBL: X05314; CAA28936.1; -.

DR HSSP: P01031; 1KJ5.

DR MGD: MGI:88228; C4.

DR InterPro: IPR002890; A2M_N.

DR InterPro: IPR000020; Anaphylatoxin.

DR InterPro: IPR001840; Anaphylatoxin.

DR InterPro: IPR001599; MacroglobinA2.

DR InterPro: IPR001134; Netrin_C.

DR Pfam: PF00207; A2M; 1.

DR Pfam: PF01835; A2M_N; 1.

DR Pfam: PF01821; ANATO; 1.

DR Pfam: PF01759; NTR; 1.

DR PRINTS: PR00004; ANAPHYLATOXN.

DR PRODOM: PD003264; Anaphylatoxin; 1.

DR SMART: SM00104; ANATO; 1.

DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.

DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.

DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.

FT NON TER

SO SEQUENCE 1148 AA; 127361 MW; 2710ECF832B6FC9 CRC64;

Query Match 49.6%; Score 56.5; DB 11; Length 1148;

Best Local Similarity 57.1%; Pred. No. 0.99;

Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDGSVNNDETCEORAR 20

DB 110 CCYDGSVNNDETCEORAR 130

RESULT 3

ID 070346 PRELIMINARY: PRT: 1738 AA.

AC 070346;

DT 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Complement C4.

GN STR19 OR C4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RA Krown L., Qin S., Lasky S.R., Loretz C., Dors M., Mahairas G.,

RA Hood L.;

RT "Sequence of the mouse major histocompatibility locus III
 region.";

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF049850; AAC05279.1; -.

DR HSSP: P01031; 1KJ5.

DR MGD: MGI:1860085; SK19.

DR MGD: MGI:88228; C4.

DR InterPro: IPR002890; A2M_N.

DR InterPro: IPR000020; Anaphylatoxin.

DR InterPro: IPR001840; Anaphylatoxin.

DR InterPro: IPR001599; MacroglobinA2.

DR InterPro: IPR001134; Netrin_C.

DR Pfam: PF00207; A2M; 1.

DR Pfam: PF01835; A2M_N; 1.

DR Pfam: PF01821; ANATO; 1.

DR Pfam: PF01759; NTR; 1.

DR PRINTS: PR00004; ANAPHYLATOXN.

DR PRODOM: PD003264; Anaphylatoxin; 1.

DR SMART: SM00104; ANATO; 1.

DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.

DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.

DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.

SO SEQUENCE 1738 AA; 192944 MW; BDD82802091EE81 CRC64;

Query Match 49.6%; Score 56.5; DB 11; Length 1738;

Best Local Similarity 57.1%; Pred. No. 1.6;

Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

OY 1 CCYDGSVNNDETCEORAR 20

DB 700 CCYDGSVNNDETCEORAR 720

RESULT 4

ID 09V174 PRELIMINARY: PRT: 608 AA.

AC 09V174;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE CG10055 protein.

GN CG10055.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

[1]

SEQUENCE FROM N.A.

RA STRAIN-BERKELEY.

RA MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chape M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Adl J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Bokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Genter A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,

RA Jajall M., Kalush F., Karen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weisslock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003672; AAF54051.1; -;
 DR FLYBASE: FBgn0037482; CC10055.
 SQ SEQUENCE 608 AA; 69145 MW; 0357365F2567014 CRC64;

Query Match 44.7%; Score 51; DB 5; Length 608;
 Best Local Similarity 57.1%; Pred. No. 4.2;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 CYDGASVNDNDETC 15
 DB 327 CYDVRTTNEPTCE 340

RESULT 5

O98977 PRELIMINARY; PRT; 1614 AA.

AC O98977;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Complement component C3-3 (Fragment).
 OS *Oncorhynchus mykiss* (Rainbow trout) (*Salmo gairdneri*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=96323260; PubMed=8710907;
 RA Sunyer J.O., Zarkadis I.K., Sahu A., Lambiris J.D.;
 RT "Multiple forms of complement C3 in trout that differ in binding to
 complement activators.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8546-8551(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=20437839; PubMed=10980316;
 RA Zarkadis I.K., Sarras M.R., Styroera G., Sunyer J.O., Lambiris J.D.;
 RT "Cloning and structure of three rainbow trout C3 molecules: a
 plausible explanation for their functional diversity.";
 RL Dev. Comp. Immunol. 25:11-24(2001).
 DR EMBL: U61753; AAC60015.2; -;
 DR HSSP: P01024; IC3D
 DR InterPro: IPR002890; A2M_N.
 DR InterPro: IPR000020; Anaphylatoxin.
 DR InterPro: IPR001840; Anaphylatoxin.
 DR InterPro: IPR001599; MacroglobulinA2.
 DR InterPro: IPR001134; Netrin_C.
 DR Pfam: PF00207; A2M_1.
 DR Pfam: PF01835; A2M_N_1.
 DR Pfam: PF01821; ANATO_1.
 DR Pfam: PF01759; NTR_1.
 DR PRINTS: PR00004; ANAPHYLATOXN.
 DR PRODOM: PD003264; Anaphylatoxin_1.
 DR SMART: SM00104; ANATO_1.
 DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.

DR PROSITE: PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE: PS01178; ANAPHYLATOXIN_2; 1.
 FT NON_TER
 SQ SEQUENCE 1614 AA; 180714 MW; 0910CE3B73D38F10 CRC64;

Query Match 44.3%; Score 50.5; DB 13; Length 1614;
 Best Local Similarity 57.9%; Pred. No. 15;
 Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

OY 1 CCYDGASVNDNDETCORA 18
 DB 640 CCMGKRNILDTYCERRA 658

RESULT 6

O9N497 PRELIMINARY; PRT; 548 AA.

AC O9N497;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Hypothetical 60.1 kDa protein.
 GN Y110A2AL.2.
 OS *Caenorhabditis elegans*.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Smith A.;
 RT "The sequence of *C. elegans* cosmid Y110A2AL.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC024746; AAF60400.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 548 AA; 60123 MW; C63EC1D429E74989 CRC64;

Query Match 43.4%; Score 49.5; DB 5; Length 548;
 Best Local Similarity 47.4%; Pred. No. 6.7;
 Matches 9; Conservative 3; Mismatches 2; Indels 5; Gaps 1;

OY 1 CC-----YDGASVNDNDETC 14
 DB 171 CCAKRDVFGSSNRNDETC 189

RESULT 7

O65686 PRELIMINARY; PRT; 135 AA.

AC O65686;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Hypothetical 15.0 kDa protein.
 OS Beet necrotic yellow vein virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 OX NCBI_TaxID=31721;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=F2;
RA Bouzouba S., Guilley H., Jonard G., Richards K., Putz C.;
RT "nucleotide sequence analysis of rna-3 and rna-4 of beet necrotic
RT yellow vein virus isolates F2 and g1.";
RL J. Gen. Virol. 66:1553-1564(1985).
DR EMBL: M36896; AAA69656.1; -.
KW Hypothetical protein.
SQ SEQUENCE 135 AA; 15027 MW; 79E2231BA5240226 CRC64;

Query Match 42.1%; Score 48; DB 12; Length 135;
Best Local Similarity 57.1%; Pred. No. 2.6;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETC 15
Db 115 CYSQVDVLSDELCE 128

RESULT 8

ID 09DS5 PRELIMINARY; PRT; 282 AA.
AC 09DS5;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical 32.1 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KAS3; AND KAS2;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennfors B.L.;
RT "Molecular analyses of European A, B and P type sources of Beet
RT necrotic yellow vein virus and detection of the rare P type in
RT Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).
DR EMBL: AF197557; AAG37097.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 32111 MW; F8D90D3208FB5C1B CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETC 15
Db 115 CYSQVDVLSDELCE 128

RESULT 9

ID 09DS4 PRELIMINARY; PRT; 282 AA.
AC 09DS4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical 32.1 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F75; AND F72;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennfors B.L.;
RT "Molecular analyses of European A, B and P type sources of Beet
RT necrotic yellow vein virus and detection of the rare P type in
RT Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).
DR EMBL: AF197548; AAG37084.1; -.

DR EMBL: AF197546; AAG37078.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 32053 MW; F8DB465FBC6B5C1B CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETC 15
Db 115 CYSQVDVLSDELCE 128

RESULT 10

ID 09DS85 PRELIMINARY; PRT; 282 AA.
AC 09DS85;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical 31.9 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D71;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennfors B.L.;
RT "Molecular analyses of European A, B and P type sources of Beet
RT necrotic yellow vein virus and detection of the rare P type in
RT Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).
DR EMBL: AF197544; AAG37076.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 31939 MW; 3383394A3A739FZD CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETC 15
Db 115 CYSQVDVLSDELCE 128

RESULT 11

ID 09DS75 PRELIMINARY; PRT; 282 AA.
AC 09DS75;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Hypothetical 32.0 kDa protein.
OS Beet necrotic yellow vein virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
OX NCBI_TaxID=31721;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=I12;
RX MEDLINE=20456802; PubMed=11003469;
RA Koenig R., Lennfors B.L.;
RT "Molecular analyses of European A, B and P type sources of Beet
RT necrotic yellow vein virus and detection of the rare P type in
RT Kazakhstan.";
RL Arch. Virol. 145:1561-1570(2000).
DR EMBL: AF197552; AAG37088.1; -.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 32024 MW; A463D478D475CF05 CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNDDETC 15
 DB 115 CYSQVDSDELCE 128

RESULT 12

Q9DS67 PRELIMINARY; PRT; 282 AA.
 AC Q9DS67;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Hypothetical 31.9 kDa protein.
 OS Beet necrotic yellow vein virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 OX NCBI_TaxID=31721;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N7;
 RX MEDLINE=20456802; PubMed=11003469;
 RA Koenig R., Lennfors B.L.;
 RT "Molecular analyses of European A, B and P type sources of Beet necrotic yellow vein virus and detection of the rare P type in Kazakhstan."
 RL Arch. Virol. 145:1561-1570(2000).
 DR EMBL; AF197559; AAC37099.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 282 AA; 31948 MW; 58A34878C68131F CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
 Best Local Similarity 57.1%; Pred. No. 5.9;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNDDETC 15
 DB 115 CYSQVDSDELCE 128

RESULT 13

Q65670 PRELIMINARY; PRT; 282 AA.
 AC Q65670;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE 31k protein.
 OS Beet necrotic yellow vein virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Benyvirus.
 OX NCBI_TaxID=31721;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S;
 RX MEDLINE=97128991; PubMed=8973531;
 RA Saito M., Kiguchi T., Kusume T., Tamada T.;
 RT "Complete nucleotide sequence of the Japanese isolate S of beet necrotic yellow vein virus RNA and comparison with European isolates."
 RL Arch. Virol. 141:2163-2175(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C;
 RX MEDLINE=97128991; PubMed=8973531;
 RA Yu J., Han C., Yang L., Li D., Liu Y.;
 RT "cDNA cloning, sequencing and expression of RNA4 from beet necrotic yellow vein virus."
 RL Acta Microbiol. Sin. 37:7-14(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C;
 RX MEDLINE=97128991; PubMed=8973531;
 RA Li D.;
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; D84413; BAA12347.1; -.
 DR EMBL; AJ239199; CAA15427.1; -.

SQ SEQUENCE 282 AA; 31970 MW; D96A3B079E063E6 CRC64;

Query Match 42.1%; Score 48; DB 12; Length 282;
 Best Local Similarity 57.1%; Pred. No. 5.9;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 CYDGASVNDDETC 15
 DB 115 CYSQVDSDELCE 128

RESULT 14

Q9DDV9 PRELIMINARY; PRT; 1684 AA.
 AC Q9DDV9;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Complement component C3-4 (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20437839; PubMed=10980316;
 RA Zaratadis I.K., Sarrias M.R., Stryer G., Sunyer J.O., Lambiris J.D.;
 RT "Cloning and structure of three rainbow trout C3 molecules: a plausible explanation for their functional diversity."
 RL Dev. Comp. Immunol. 25:11-24(2001).
 DR EMBL; AF271080; AAC40610.1; -.
 DR HSSP; P01024; IC3D

DR InterPro; IPR002890; A2M_N
 DR InterPro; IPR000020; Anaphylatoxin.
 DR InterPro; IPR001599; MacroglobinA2.
 DR InterPro; IPR001134; Neutrin_C.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00207; A2M; 1.
 DR Pfam; PF01835; A2M_N; 1.
 DR Pfam; PF01821; ANATO; 1.
 DR Pfam; PF01759; NTR; 1.
 DR ProDom; PD003264; Anaphylatoxin; 1.
 DR SMART; SM00104; ANATO; 1.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
 DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 FT NON_TER 1
 FT TER 1684
 SQ SEQUENCE 1684 AA; 189500 MW; 903802CNAAE4D20D CRC64;

Query Match 41.7%; Score 47.5; DB 13; Length 1684;
 Best Local Similarity 55.0%; Pred. No. 4.9;
 Matches 11; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

OY 1 CCYDGASVNN--DECEORA 18
 DB 717 CCMQDMR-NMILDYTCERRS 735

RESULT 15

Q9GT77 PRELIMINARY; PRT; 227 AA.
 AC Q9GT77;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Ookinete surface antigen-like protein Pf528.
 OS Plasmodium yoelii nigeriensis.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=31274;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=20520976; PubMed=11071297;
RA Taylor D., Cloonan N., Mann V., Cheng Q., Saul A.;
PT "Sequence diversity in rodent malaria of the Pfs28 ookinete surface
antigen homologs.";
RL Mol. Biochem. Parasitol. 110:429-434(2000).
DR EMBL; AF232055; AAC27295.1; -;
DR InterPro; IPR000561; EGF-like.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 227 AA; 2421 MW; A791B0A4E795017 CRC64;

Query Match 41.2%; Score 47; DB 5; Length 227;
Best Local Similarity 46.7%; Pred. NO. 6.8;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 CYDGASVNNDETCQ 16
| | : | : | | :
Db 46 CIDGYGLKNNTCEK 60

Search completed: May 1, 2003, 22:19:15
Job time : 86 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:08:56 ; Search time 36 Seconds
(without alignments)
74,028 Million cell updates/sec

Title: US-09-651-685A-5
Perfect score: 114
Sequence: 1 CCYDGASVNNDFCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	22	AAB74055
2	114	100.0	64	18	AAW07784
3	114	100.0	65	18	AAW07785
4	114	100.0	66	18	AAW07786
5	114	100.0	67	18	AAW07787
6	114	100.0	68	18	AAW07788
7	114	100.0	69	18	AAW07789
8	114	100.0	70	18	AAW07790
9	114	100.0	71	18	AAW07792
10	114	100.0	71	18	AAW07783

11	114	100.0	71	18	AAW07804	Human complement C
12	114	100.0	71	18	AAW07791	Human complement C
13	114	100.0	72	18	AAW07792	Human complement C
14	114	100.0	74	22	AAB74053	Human C5a. Homo s
15	111	97.4	20	22	AAB74111	C-terminal truncat
16	110	96.5	20	22	AAB74110	C-terminal truncat
17	110	96.5	20	22	AAB74112	C-terminal truncat
18	110	96.5	20	22	AAB74113	C-terminal truncat
19	110	96.5	20	22	AAB74114	C-terminal truncat
20	110	96.5	20	22	AAB74116	C-terminal truncat
21	110	96.5	74	22	AAB74119	Variant human C5a.
22	109	95.6	19	22	AAB74097	C-terminal truncat
23	109	95.6	20	22	AAB74120	Human C5a peptide
24	109	95.6	74	8	AAW71666	Human anaphylatoxi
25	109	95.6	74	16	AAW75497	Human C5a protein.
26	109	95.6	74	20	AAW959580	Solid phase sequen
27	109	95.6	74	22	AAE05454	Human C5a anaphyla
28	109	95.6	1675	16	AAB77604	Pro-C5 polypeptide
29	108	94.7	20	22	AAB74107	C-terminal truncat
30	108	94.7	20	22	AAB74108	C-terminal truncat
31	106	93.0	20	22	AAB74115	C-terminal truncat
32	105	92.1	18	22	AAB74098	C-terminal truncat
33	105	92.1	19	22	AAB74102	C-terminal truncat
34	102	89.5	20	22	AAB74109	C-terminal truncat
35	101	88.6	17	22	AAB74099	C-terminal truncat
36	98	86.0	20	22	AAB74117	C-terminal truncat
37	96	84.2	16	22	AAB74100	C-terminal truncat
38	96	84.2	18	22	AAB74103	C-terminal truncat
39	94	82.5	74	22	AAE05456	Cow C5a anaphylato
40	94	82.5	74	22	AAB74057	Bovine C5a. Bos s
41	93	81.6	74	22	AAE05455	Pig C5a anaphylato
42	93	81.6	74	22	AAB74058	Porcine C5a. Sus
43	91	79.8	15	22	AAB74101	C-terminal truncat
44	89	78.1	17	22	AAB74104	C-terminal truncat
45	88	77.2	77	22	AAE05458	Mouse C5a anaphyla

ALIGNMENTS

RESULT 1
AAB74055
ID AAB74055 standard; Peptide: 20 AA.
XX
AC AAB74055;
XX
DT 16-MAY-2001 (first entry)
XX
DE Human C5a peptide fragment #2.
XX
KW Human; C5a; complement; antibody; bacterial infection; sinusitis;
KW meningitis; respiratory; gastrointestinal; urinary tract infection;
KW wound; anaphylatoxin; sepsis.
XX
OS Homo sapiens.
XX
PN WO200115731-A1.
XX
PD 08-MAR-2001.
XX
PE 31-AUG-2000; 2000MO-US24219.
XX
PR 31-AUG-1999; 99US-0387671.
XX
PA (UNMI) UNIV MICHIGAN.
XX
PI Ward PA, Huber-Lang M, Sarma V,
XX
DR WPI; 2001-226665/23.
XX
PT N-PSDB; AAF75793.
PT
Compositions for treating blood-borne and toxin mediated diseases and
treatment of sepsis in humans and other animals comprises anti-C5a

PT antibodies generated against C-terminal truncated C5a peptides
 XX
 PS Claim 8; Page 26; 84pp: English.
 XX
 CC The present sequence is a peptide fragment of human complement component
 CC C5a (the full-length sequence is given in AAB74053). The present
 CC invention relates to an antibody specific for the present sequence. The
 CC C5a-antibody can be used in a therapeutic composition, which is useful
 CC for treating a subject suffering from bacterial infection, e.g.
 CC infections, meningitis, respiratory, gastrointestinal or urinary tract
 CC infections or infections in wounds. In addition, the C5a antibody can
 CC be used for treating sepsis. C5a is also known as anaphylatoxin.
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 114; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.5e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCYDGASVNNDETCERAR 20
 11111111111111111111
 Db 1 CCYDGASVNNDETCERAR 20

RESULT 2

AAW07784
 ID AAW07784 standard; protein; 64 AA.
 XX
 AC AAW07784;
 XX
 DT 01-SEP-1997 (first entry)
 XX

DE Human complement C5a protein derivative analogue 1.
 XX

KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
 KW treatment; prevention; disease; inflammation; pneumonitis; burn;
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
 KW post myocardial; infarction; inflammatory bowel; endotoxic shock;
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 KW immunosuppressive therapy; blood transfusion; dysfunction;
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

FT Key Location/Qualifiers
 FT MISC-difference 1

FT MISC-difference 27 /note= "wild type Thr replaced by Met"
 FT MISC-difference 64 /note= "wild type Cys replaced by Ser"

FT MISC-difference 64 /note= "wild type Asn replaced by Cys"
 XX

PN WO9639503-A1.
 XX

PD 12-DEC-1996.
 XX

PF 04-JUN-1996; 96WO-EP02422.
 XX

PR 05-JUN-1995; 95US-0463377.
 PR 05-JUN-1995; 95US-0462648.
 PR 05-JUN-1995; 95US-0463224.
 XX

PA (CIBA) CIBA GEIGY AG.
 XX

PI Schmitz A, Van Heeke G, Van Oostrum J;
 XX

DR WPI; 1997-043125/04.
 XX

PT New human complement C5a poly-peptide derivs. - used as C5a receptor
 PT antagonists, partic. for treating C5a-mediated diseases and
 PT inflammatory conditions
 XX

PS Example 3; Page -, 93pp: English.
 XX

CC The present sequence, the human complement C5a derivative 1-64,
 CC Thrlmet, Cys27Ser, Asn64Cys, is a C5a receptor antagonist which
 CC exhibits no agonist activity. It can be used to treat or prevent
 CC C5a mediated diseases or inflammation, e.g. pneumonitis, adult
 CC respiratory distress syndrome (ARDS), pulmonary inflammation or
 CC injury, post myocardial infarction inflammation, inflammatory bowel
 CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
 CC severe trauma and burns. It can also be used to treat patients
 CC suffering from transplant rejection, receiving immunosuppressive
 CC therapy or massive blood transfusion, exposed to medical devices
 CC or experiencing pulmonary dysfunction following haemodialysis or
 CC leukopheresis. It can also be used as a prophylactic, particularly
 CC in conditions caused by reperfusion, e.g. reperfusion following
 CC ischaemia, and circulatory contact with medical devices, as well as
 CC to prevent transplant rejection.
 CC Antibodies against the derivative can be used to detect or quantify
 CC the derivative and modify, e.g. neutralise, its activity in vivo.
 CC N.B. Sequence not given in specification, but constructed using the
 CC wild type sequence given on pages 51-52.
 XX

SQ Sequence 64 AA;
 Query Match 100.0%; Score 114; DB 18; Length 64;
 Best Local Similarity 100.0%; Pred. No. 1.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCYDGASVNNDETCERAR 20
 11111111111111111111
 Db 21 CCYDGASVNNDETCERAR 40

RESULT 3

AAW07785
 ID AAW07785 standard; protein; 65 AA.
 XX

AC AAW07785;
 XX

DT 01-SEP-1997 (first entry)
 XX

DE Human complement C5a protein derivative analogue 2.
 XX

KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
 KW treatment; prevention; disease; inflammation; pneumonitis; burn;
 KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
 KW post myocardial; infarction; inflammatory bowel; endotoxic shock;
 KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
 KW immunosuppressive therapy; blood transfusion; dysfunction;
 KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

FT Key Location/Qualifiers
 FT MISC-difference 1

FT MISC-difference 27 /note= "wild type Thr replaced by Met"
 FT MISC-difference 65 /note= "wild type Cys replaced by Ser"

FT MISC-difference 65 /note= "wild type Ile replaced by Cys"
 XX

PN WO9639503-A1.
 XX

PD 12-DEC-1996.
 XX

PF 04-JUN-1996; 96WO-EP02422.
 XX

PR 05-JUN-1995; 95US-0463377.
 PR 05-JUN-1995; 95US-0462648.
 PR 05-JUN-1995; 95US-0463224.
 XX

PA (CIBA) CIBA GEIGY AG.
 XX

```

XX PI Schmitz A, Van Heeke G, Van Oostrum J;
XX DR WPI: 1997-043125/04.
XX PT New human complement C5a poly-peptide derivs. - used as C5a receptor
XX PT antagonists, partic. for treating C5a-mediated diseases and
XX PT inflammatory conditions
XX PS Example 3; Page -: 93pp; English.
XX CC The present sequence, the human complement C5a derivative 1-65,
XX CC Thrlmet, Cys27Ser, Ile65Cys, is a C5a receptor antagonist which
XX CC exhibits no agonist activity. It can be used to treat or prevent
XX CC C5a mediated diseases or inflammation, e.g. pneumonia, adult
XX CC respiratory distress syndrome (ARDS), pulmonary inflammation or
XX CC injury, post myocardial infarction inflammation, inflammatory bowel
XX CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX CC severe trauma and burns. It can also be used to treat patients
XX CC suffering from transplant rejection, receiving immunosuppressive
XX CC therapy or massive blood transfusion, exposed to medical devices
XX CC or experiencing pulmonary dysfunction following haemodialysis or
XX CC leukopheresis. It can also be used as a prophylactic, particularly
XX CC in conditions caused by reperfusion, e.g. reperfusion following
XX CC ischaemia, and circulatory contact with medical devices, as well as
XX CC to prevent transplant rejection.
XX CC Antibodies against the derivative can be used to detect or quantify
XX CC the derivative and modify, e.g. neutralise, its activity in vivo.
XX CC N.B. Sequence not given in specification, but constructed using the
XX CC wild type sequence given on pages 51-52.
XX SO Sequence 65 AA:
XX
XX Query Match 100.0%; Score 114; DB 18; Length 65;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCYDGASVNDTCQRRAR 20
Dd 21 CCYDGASVNDTCQRRAR 40

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PD 12-DEC-1996.
XX 04-JUN-1996; 96WO-EP02422.
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX (CIBA ) CIBA GEIGY AG.
XX PI Schmitz A, Van Heeke G, Van Oostrum J;
XX DR WPI: 1997-043125/04.
XX PT New human complement C5a poly-peptide derivs. - used as C5a receptor
XX PT antagonists, partic. for treating C5a-mediated diseases and
XX PT inflammatory conditions
XX PS Example 3; Page -: 93pp; English.
XX CC The present sequence, the human complement C5a derivative 1-66,
XX CC Thrlmet, Cys27Ser, Ser66Cys, is a C5a receptor antagonist which
XX CC exhibits no agonist activity. It can be used to treat or prevent
XX CC C5a mediated diseases or inflammation, e.g. pneumonia, adult
XX CC respiratory distress syndrome (ARDS), pulmonary inflammation or
XX CC injury, post myocardial infarction inflammation, inflammatory bowel
XX CC disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX CC severe trauma and burns. It can also be used to treat patients
XX CC suffering from transplant rejection, receiving immunosuppressive
XX CC therapy or massive blood transfusion, exposed to medical devices
XX CC or experiencing pulmonary dysfunction following haemodialysis or
XX CC leukopheresis. It can also be used as a prophylactic, particularly
XX CC in conditions caused by reperfusion, e.g. reperfusion following
XX CC ischaemia, and circulatory contact with medical devices, as well as
XX CC to prevent transplant rejection.
XX CC Antibodies against the derivative can be used to detect or quantify
XX CC the derivative and modify, e.g. neutralise, its activity in vivo.
XX CC N.B. Sequence not given in specification, but constructed using the
XX CC wild type sequence given on pages 51-52.
XX SO Sequence 66 AA:
XX
XX Query Match 100.0%; Score 114; DB 18; Length 66;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCYDGASVNDTCQRRAR 20
Dd 21 CCYDGASVNDTCQRRAR 40

```

```

RESULT 4
AAW07786
ID AAW07786 standard; protein; 66 AA.
XX AC AAW07786;
XX 01-SEP-1997 (first entry)
XX DE Human complement C5a protein derivative analogue 3.
XX KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
XX KW treatment; prevention; disease; inflammation; pneumonia; burn;
XX KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
XX KW post myocardial infarction; inflammation; inflammatory bowel; endotoxic shock;
XX KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
XX KW immunosuppressive therapy; blood transfusion; dysfunction;
XX KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT MISC-difference 1
XX FT MISC-difference 27 /note- "wild type Thr replaced by Met"
XX FT MISC-difference 66 /note- "wild type Cys replaced by Ser"
XX FT MISC-difference /note- "wild type Ser replaced by Cys"
XX PN W09639503-A1.
XX

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RESULT 5
AAW07787
ID AAW07787 standard; protein; 67 AA.
XX AC AAW07787;
XX 01-SEP-1997 (first entry)
XX DE Human complement C5a protein derivative analogue 4.
XX KW Human; complement; C5a; derivative; receptor; antagonist; trauma;
XX KW treatment; prevention; disease; inflammation; pneumonia; burn;
XX KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
XX KW post myocardial infarction; inflammation; inflammatory bowel; endotoxic shock;
XX KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
XX KW immunosuppressive therapy; blood transfusion; dysfunction;
XX KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX

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FT MISC-difference 1
FT /note= "wild type Thr replaced by Met"
FT MISC-difference 27
FT /note= "wild type Cys replaced by Ser"
FT MISC-difference 67
FT /note= "wild type His replaced by Cys"
XX
XX WO9639503-A1.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
XX
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Schmitz A, Van Heeke G, Van Oostrum J;
XX WPI; 1997-043125/04.
XX
XX New human complement C5a polypeptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -: 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-67,
XX ThrlMet, Cys27Ser, His67Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonitis, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leukopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischaemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 67 AA:
XX
XX Query Match 100.0%; Score 114; DB 18; Length 67;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 0Y 1 CCYDGASVNNDETCEGRAR 20
XX ||||||||||||||||
XX 21 CCYDGASVNNDETCEGRAR 40
XX
XX RESULT 6
XX AAW07788 standard; protein; 68 AA.
XX
XX AC AAW07788;
XX
XX 01-SEP-1997 (first entry)
XX
XX Human; complement C5a protein derivative analogue 5.
XX
XX Human; complement; C5a; derivative; receptor; antagonist; trauma;
XX treatment; prevention; disease; inflammation; pneumonitis; burn;
XX adult respiratory distress syndrome; ARDS; pulmonary; injury;

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KW post myocardial; infarction; inflammatory bowel; endotoxic shock;
KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
KW immunosuppressive therapy; blood transfusion; dysfunction;
KW haemodialysis; leukopheresis; prophylaxis; reperfusion.
XX
XX Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX MISC-difference 1
XX /note= "wild type Thr replaced by Met"
XX MISC-difference 27
XX /note= "wild type Cys replaced by Ser"
XX MISC-difference 68
XX /note= "wild type Lys replaced by Cys"
XX
XX WO9639503-A1.
XX
XX 12-DEC-1996.
XX
XX 04-JUN-1996; 96WO-EP02422.
XX
XX 05-JUN-1995; 95US-0463377.
XX 05-JUN-1995; 95US-0462648.
XX 05-JUN-1995; 95US-0463224.
XX
XX (CIBA ) CIBA GEIGY AG.
XX
XX Schmitz A, Van Heeke G, Van Oostrum J;
XX WPI; 1997-043125/04.
XX
XX New human complement C5a polypeptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions
XX
XX Example 3; Page -: 93pp; English.
XX
XX The present sequence, the human complement C5a derivative 1-68,
XX ThrlMet, Cys27Ser, Lys68Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonitis, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients
XX suffering from transplant rejection, receiving immunosuppressive
XX therapy or massive blood transfusion, exposed to medical devices
XX or experiencing pulmonary dysfunction following haemodialysis or
XX leukopheresis. It can also be used as a prophylactic, particularly
XX in conditions caused by reperfusion, e.g. reperfusion following
XX ischaemia, and circulatory contact with medical devices, as well as
XX to prevent transplant rejection.
XX Antibodies against the derivative can be used to detect or quantify
XX the derivative and modify, e.g. neutralise, its activity in vivo.
XX N.B. Sequence not given in specification, but constructed using the
XX wild type sequence given on pages 51-52.
XX
XX Sequence 68 AA:
XX
XX Query Match 100.0%; Score 114; DB 18; Length 68;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-10;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 0Y 1 CCYDGASVNNDETCEGRAR 20
XX ||||||||||||||||
XX 21 CCYDGASVNNDETCEGRAR 40
XX
XX RESULT 7
XX AAW07789 standard; protein; 69 AA.
XX
XX ID AAW07789
XX

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AAW07789;
 01-SEP-1997 (first entry)
 Human complement C5a protein derivative analogue 6.
 Human: complement; C5a: derivative; receptor; antagonist; trauma; treatment; prevention; disease; inflammation; pneumonia; burn; adult respiratory distress syndrome; ARDS; pulmonary; injury; post myocardial; infarction; inflammatory bowel; endotoxic shock; rheumatoid arthritis; psoriasis; sepsis; transplant rejection; immunosuppressive therapy; blood transfusion; dysfunction; haemodialysis; leukopheresis; prophylaxis; reperfusion.
 Homo sapiens.
 Synthetic.
 Key
 MISC-difference 1 Location/Qualifiers
 FT MISC-difference 1 /note= "wild type Thr replaced by Met"
 FT MISC-difference 27 /note= "wild type Cys replaced by Ser"
 FT MISC-difference 69 /note= "wild type Asp replaced by Cys"
 MO9639503-A1.
 12-DEC-1996.
 04-JUN-1996; 96MO-EP02422.
 05-JUN-1995; 95US-0463377.
 05-JUN-1995; 95US-0462648.
 05-JUN-1995; 95US-0463224.
 (CIBA) CIBA GEIGY AG.
 Schmitz A, Van Heeke G, Van Oostrum J;
 WPI; 1997-043125/04.
 New human complement C5a poly-peptide derivs. - used as C5a receptor antagonists, partic. for treating C5a-mediated diseases and inflammatory conditions
 Example 3; Page -: 93pp; English.
 The present sequence, the human complement C5a derivative 1-69, Thr1Met, Cys27Ser, Asp69Cys, is a C5a receptor antagonist which exhibits no agonist activity. It can be used to treat or prevent C5a mediated diseases or inflammation, e.g. pneumonia, adult respiratory distress syndrome (ARDS), pulmonary inflammation or injury, post myocardial infarction inflammation, inflammatory bowel disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis, severe trauma and burns. It can also be used to treat patients suffering from transplant rejection, receiving immunosuppressive therapy or massive blood transfusion, exposed to medical devices or leukopheresis. It can also be used as a prophylactic, particularly in conditions caused by reperfusion, e.g. reperfusion following ischemia, and circulatory contact with medical devices, as well as to prevent transplant rejection.
 Antibodies against the derivative can be used to detect or quantify the derivative and modify, e.g. neutralise, its activity in vivo.
 N.B. Sequence not given in specification, but constructed using the wild type sequence given on pages 51-52.
 Sequence 69 AA:
 Query Match 100.0%; Score 114; DB 18; Length 69;
 Best Local Similarity 100.0%; Pred No. 1.8e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTCGEORAR 20
 DB 21 CCYDGASVNDTCGEORAR 40
 RESULT 8
 AAW07790
 ID AAW07790 standard; protein: 70 AA.
 AAW07790;
 01-SEP-1997 (first entry)
 Human complement C5a protein derivative analogue 7.
 Human: complement; C5a: derivative; receptor; antagonist; trauma; treatment; prevention; disease; inflammation; pneumonia; burn; adult respiratory distress syndrome; ARDS; pulmonary; injury; post myocardial; infarction; inflammatory bowel; endotoxic shock; rheumatoid arthritis; psoriasis; sepsis; transplant rejection; immunosuppressive therapy; blood transfusion; dysfunction; haemodialysis; leukopheresis; prophylaxis; reperfusion.
 Homo sapiens.
 Synthetic.
 Key
 MISC-difference 1 Location/Qualifiers
 FT MISC-difference 1 /note= "wild type Thr replaced by Met"
 FT MISC-difference 27 /note= "wild type Cys replaced by Ser"
 FT MISC-difference 70 /note= "wild type Met replaced by Cys"
 MO9639503-A1.
 12-DEC-1996.
 04-JUN-1996; 96MO-EP02422.
 05-JUN-1995; 95US-0463377.
 05-JUN-1995; 95US-0462648.
 05-JUN-1995; 95US-0463224.
 (CIBA) CIBA GEIGY AG.
 Schmitz A, Van Heeke G, Van Oostrum J;
 WPI; 1997-043125/04.
 New human complement C5a poly-peptide derivs. - used as C5a receptor antagonists, partic. for treating C5a-mediated diseases and inflammatory conditions
 Example 3; Page -: 93pp; English.
 The present sequence, the human complement C5a derivative 1-70, Thr1Met, Cys27Ser, Met70Cys, is a C5a receptor antagonist which exhibits no agonist activity. It can be used to treat or prevent C5a mediated diseases or inflammation, e.g. pneumonia, adult respiratory distress syndrome (ARDS), pulmonary inflammation or injury, post myocardial infarction inflammation, inflammatory bowel disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis, severe trauma and burns. It can also be used to treat patients suffering from transplant rejection, receiving immunosuppressive therapy or massive blood transfusion, exposed to medical devices or leukopheresis. It can also be used as a prophylactic, particularly in conditions caused by reperfusion, e.g. reperfusion following ischemia, and circulatory contact with medical devices, as well as to prevent transplant rejection.
 Antibodies against the derivative can be used to detect or quantify the derivative and modify, e.g. neutralise, its activity in vivo.

CC N.B. Sequence not given in specification, but constructed using the
CC wild type sequence given on pages 51-52.

XX Sequence 70 AA;

Query Match 100.0%; Score 114; DB 18; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDASVNNDETCEORAR 20
|
DB 21 CCYDASVNNDETCEORAR 40

RESULT 9
AAW07782

ID AAW07782 standard; protein; 71 AA.

AC AAW07782;

XX 01-SEP-1997 (first entry)

DE Human complement C5a protein derivative.

XX Human; complement; C5a; derivative; receptor; antagonist; trauma;
KW treatment; prevention; disease; inflammation; pneumonitis; burn;
KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
KW post myocardial; infarction; inflammatory bowel; endotoxic shock;
KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
KW immunosuppressive therapy; blood transfusion; dysfunction;
KW haemodialysis; leukopheresis; prophylaxis; reperfusion.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "wild type Thr replaced by Gly"

FT Misc-difference 27 /note= "wild type Cys replaced by Ser"

FT Misc-difference 71 /note= "wild type Gln replaced by Cys"

XX W09639503-A1.

PD 12-DEC-1996.

XX 04-JUN-1996; 96WO-EP02422.

XX 05-JUN-1995; 95US-0463377.

PR 05-JUN-1995; 95US-0462648.

PR 05-JUN-1995; 95US-0463224.

XX (CIBA) CIBA GEIGY AG.

XX Schmitz A, Van Heeke G, Van Oostrum J;

XX WPI; 1997-043125/04.

XX New human complement C5a poly-peptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions

XX Claim 11: Page -; 93pp: English.

XX The present sequence, the human complement C5a derivative 1-71,
XX Thirily, Cys27Ser, Gln71Cys, is a C5a receptor antagonist which
XX exhibits no agonist activity. It can be used to treat or prevent
XX C5a mediated diseases or inflammation, e.g. pneumonitis, adult
XX respiratory distress syndrome (ARDS), pulmonary inflammation or
XX injury, post myocardial infarction inflammation, inflammatory bowel
XX disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
XX severe trauma and burns. It can also be used to treat patients

CC suffering from transplant rejection, receiving immunosuppressive
CC therapy or massive blood transfusion, exposed to medical devices
CC or experiencing pulmonary dysfunction following haemodialysis or
CC leukopheresis. It can also be used as a prophylactic, particularly
CC in conditions caused by reperfusion, e.g. reperfusion following
CC ischaemia, and circulatory contact with medical devices, as well as
CC to prevent transplant rejection.
CC Antibodies against the derivative can be used to detect or quantify
CC the derivative and modify, e.g. neutralise, its activity in vivo.
CC N.B. Sequence not given in specification, but constructed using the
CC wild type sequence given on pages 51-52.

XX Sequence 71 AA;

Query Match 100.0%; Score 114; DB 18; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDASVNNDETCEORAR 20
|
DB 21 CCYDASVNNDETCEORAR 40

RESULT 10
AAW07783

ID AAW07783 standard; protein; 71 AA.

AC AAW07783;

XX 01-SEP-1997 (first entry)

DE Human complement C5a protein derivative.

XX Human; complement; C5a; derivative; receptor; antagonist; trauma;
KW treatment; prevention; disease; inflammation; pneumonitis; burn;
KW adult respiratory distress syndrome; ARDS; pulmonary; injury;
KW post myocardial; infarction; inflammatory bowel; endotoxic shock;
KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;
KW immunosuppressive therapy; blood transfusion; dysfunction;
KW haemodialysis; leukopheresis; prophylaxis; reperfusion.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "wild type Thr replaced by Gly"

FT Misc-difference 27 /note= "wild type Cys replaced by Ser"

FT Misc-difference 67 /note= "wild type His replaced by Phe"

FT Misc-difference 71 /note= "wild type Gln replaced by Cys"

XX W09639503-A1.

PD 12-DEC-1996.

XX 04-JUN-1996; 96WO-EP02422.

XX 05-JUN-1995; 95US-0463377.

PR 05-JUN-1995; 95US-0462648.

PR 05-JUN-1995; 95US-0463224.

XX (CIBA) CIBA GEIGY AG.

XX Schmitz A, Van Heeke G, Van Oostrum J;

XX WPI; 1997-043125/04.

XX New human complement C5a poly-peptide derivs. - used as C5a receptor
XX antagonists, partic. for treating C5a-mediated diseases and
XX inflammatory conditions

XX Claim 12, page -: 93pp: English.

XX The present sequence, the human complement C5a derivative 1-71,

XX Thirily, Cys27Ser, His67Phe, Glu71Cys, is a C5a receptor antagonist

CC which exhibits no agonist activity. It can be used to treat or

CC prevent C5a mediated diseases or inflammation, e.g. pneumonia,

CC adult respiratory distress syndrome (ARDS), pulmonary inflammation

CC or injury, post myocardial infarction inflammation, inflammatory

CC bowel disease, rheumatoid arthritis, psoriasis, endotoxic shock,

CC sepsis, severe trauma and burns. It can also be used to treat

CC patients suffering from transplant rejection, receiving

CC immunosuppressive therapy or massive blood transfusion, exposed to

CC medical devices or experiencing pulmonary dysfunction following

CC haemodialysis or leukopheresis. It can also be used as a

CC prophylactic, particularly in conditions caused by reperfusion,

CC e.g. reperfusion following ischaemia, and circulatory contact with

CC medical devices, as well as to prevent transplant rejection.

CC Antibodies against the derivative can be used to detect or quantify

CC the derivative and modify, e.g. neutralise, its activity in vivo.

CC N.B. Sequence not given in specification, but constructed using the

CC wild type sequence given on pages 51-52.

XX

SQ Sequence 71 AA:

Query Match 100.0%; Score 114; DB 18; Length 71;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNDTCQRRAR 20

21 CCYDGASVNDTCQRRAR 40

Db

RESULT 11

AAW07804

ID AAW07804 standard; protein; 71 AA.

XX

AC AAW07804;

XX

DT 01-SEP-1997 (first entry)

XX

DE Human complement C5a protein derivative.

XX

KW Human; complement; C5a; derivative; receptor; antagonist; trauma;

KW treatment; prevention; disease; inflammation; pneumonia; burn;

KW adult respiratory distress syndrome; ARDS; pulmonary; injury;

KW post myocardial infarction; inflammatory bowel; endotoxic shock;

KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;

KW immunosuppressive therapy; blood transfusion; dysfunction;

KW haemodialysis; leukopheresis; prophylaxis; reperfusion.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

FT Key Location/Qualifiers

FT MISC-difference 1 /note- "wild type Thr replaced by Met"

FT MISC-difference 27 /note- "wild type Cys replaced by Ser"

FT MISC-difference 67 /note- "wild type His replaced by Phe"

FT MISC-difference 71 /note- "wild type Glu replaced by Cys"

XX

XX W09639503-A1.

XX

XX 12-DEC-1996.

XX

XX 04-JUN-1996; 96WO-EP02422.

XX

XX 05-JUN-1995; 95US-0463377.

XX

PR 05-JUN-1995; 95US-0462648.

PR 05-JUN-1995; 95US-0463224.

XX

XX (CIBA) CIBA GEIGY AG.

XX

PI Schmitz A, Van Heeke G, Van Oostrom J;

XX

XX WPI: 1997-043125/04.

XX

DR N-PSDB; AAT47209.

XX

XX New human complement C5a poly-peptide derivs. - used as C5a receptor

PT antagonists, partic. for treating C5a-mediated diseases and

PT inflammatory conditions

XX

XX Example 3; page -: 93pp: English.

XX

XX The present sequence, the human complement C5a derivative 1-71,

CC Thirly, Cys27Ser, His67Phe, Glu71Cys, is a C5a receptor antagonist

CC which exhibits no agonist activity. It can be used to treat or

CC prevent C5a mediated diseases or inflammation, e.g. pneumonia,

CC adult respiratory distress syndrome (ARDS), pulmonary inflammation

CC or injury, post myocardial infarction inflammation, inflammatory

CC bowel disease, rheumatoid arthritis, psoriasis, endotoxic shock,

CC sepsis, severe trauma and burns. It can also be used to treat

CC patients suffering from transplant rejection, receiving

CC immunosuppressive therapy or massive blood transfusion, exposed to

CC medical devices or experiencing pulmonary dysfunction following

CC haemodialysis or leukopheresis. It can also be used as a

CC prophylactic, particularly in conditions caused by reperfusion,

CC e.g. reperfusion following ischaemia, and circulatory contact with

CC medical devices, as well as to prevent transplant rejection.

CC Antibodies against the derivative can be used to detect or quantify

CC the derivative and modify, e.g. neutralise, its activity in vivo.

CC N.B. Sequence not given in specification, but constructed using the

CC wild type sequence given on pages 51-52.

XX

SQ Sequence 71 AA:

Query Match 100.0%; Score 114; DB 18; Length 71;

Best Local Similarity 100.0%; Pred. No. 1.8e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNDTCQRRAR 20

21 CCYDGASVNDTCQRRAR 40

Db

RESULT 12

AAW07791

ID AAW07791 standard; protein; 71 AA.

XX

AC AAW07791;

XX

DT 01-SEP-1997 (first entry)

XX

DE Human complement C5a protein derivative analogue 8.

XX

KW Human; complement; C5a; derivative; receptor; antagonist; trauma;

KW treatment; prevention; disease; inflammation; pneumonia; burn;

KW adult respiratory distress syndrome; ARDS; pulmonary; injury;

KW post myocardial infarction; inflammatory bowel; endotoxic shock;

KW rheumatoid arthritis; psoriasis; sepsis; transplant rejection;

KW immunosuppressive therapy; blood transfusion; dysfunction;

KW haemodialysis; leukopheresis; prophylaxis; reperfusion.

XX

OS Homo sapiens.

XX

OS Synthetic.

XX

FT Key Location/Qualifiers

FT MISC-difference 1 /note- "wild type Thr replaced by Met"

FT MISC-difference 27 /note- "wild type Cys replaced by Ser"

FT MISC-difference 71 /note- "wild type His replaced by Phe"

FT

XX Human; C5a: complement; antibody; bacterial infection; sinusitis;
 KW meningitis; respiratory; gastrointestinal; urinary tract infection;
 KM wound; anaphylatoxin; sepsis.

XX Homo sapiens.

PN MO200115731-A1.

PD 08-MAR-2001.

PF 31-AUG-2000; 2000MO-US24219.

PR 31-AUG-1999; 99US-0387671.

PA (UNMI) UNIV MICHIGAN.

PI Ward PA, Huber-Lang M, Sarma V;

DR WPI: 2001-226665/23.

DR N-PSDB; AAF75791.

PT Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides

PS Example 7; Page 26; 84pp; English.

CC The present sequence is human complement component C5a. The present
 CC invention relates to an antibody specific for the present sequence. The
 CC C5a-antibody can be used in a therapeutic composition, which is useful
 CC for treating a subject suffering from bacterial infection, e.g.
 CC sinusitis, meningitis, respiratory, gastrointestinal or urinary tract
 CC infections or infections in wounds. In addition, the C5a antibody can
 CC be used for treating sepsis. C5a is also known as anaphylatoxin.

SQ Sequence 74 AA;

Query Match 100.0%; Score 114; DB 22; Length 74;

Best Local Similarity 100.0%; Pred. No. 1.9e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETCEORAR 20

DB 21 CCYDGASVNNDETCEORAR 40

RESULT 15

AAB74111

ID AAB74111 standard; Peptide: 20 AA.

AC AAB74111;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #49.

C5a: complement; antibody; bacterial infection; sinusitis;
 KW meningitis; respiratory; gastrointestinal; urinary tract infection;
 KM wound; anaphylatoxin; sepsis.

OS Unidentified.

PN MO200115731-A1.

PD 08-MAR-2001.

PF 31-AUG-2000; 2000MO-US24219.

PR 31-AUG-1999; 99US-0387671.

PA (UNMI) UNIV MICHIGAN.

PI Ward PA, Huber-Lang M, Sarma V;

DR WPI: 2001-226665/23.

PT Compositions for treating blood-borne and toxin mediated diseases and
 PT treatment of sepsis in humans and other animals comprises anti-C5a
 PT antibodies generated against C-terminal truncated C5a peptides

PS Disclosure; Page 30; 84pp; English.

CC The present sequence is a C-terminal truncated C5a peptide fragment. The
 CC present invention relates to an antibody specific for the present
 CC sequence. The C5a-antibody can be used in a therapeutic composition,
 CC which is useful for treating a subject suffering from bacterial
 CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
 CC urinary tract infections or infections in wounds. In addition, the C5a
 CC antibody can be used for treating sepsis. C5a is also known as
 CC anaphylatoxin.

SQ Sequence 20 AA;

Query Match 97.4%; Score 111; DB 22; Length 20;

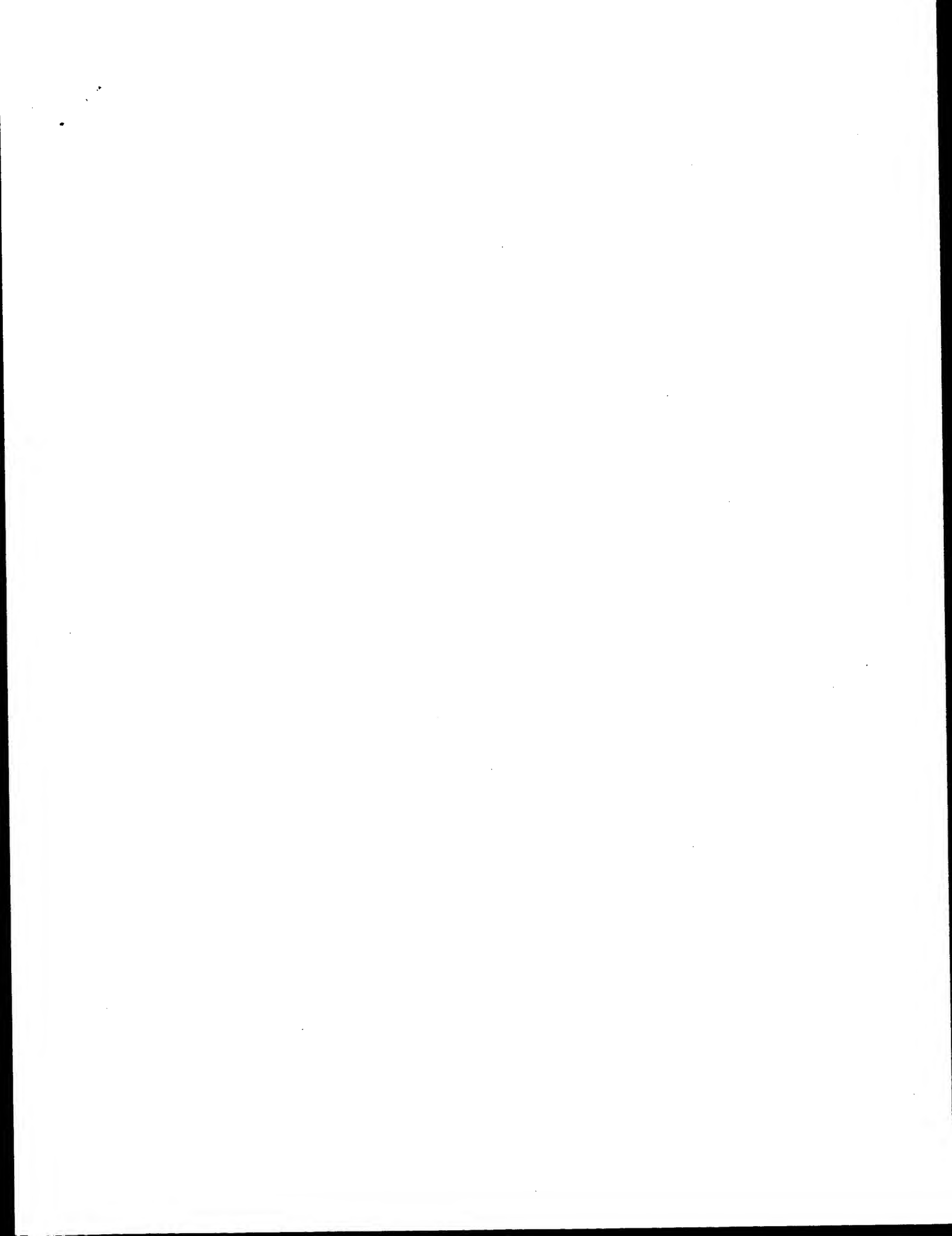
Best Local Similarity 95.0%; Pred. No. 1.3e-10;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETCEORAR 20

DB 1 CCYDGATVNNDETCEORAR 20

Search completed: May 1, 2003, 22:17:25
 Job time : 36 secs



GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 1, 2003, 22:19:22 ; Search time 16 Seconds

(Without alignments)
107.858 Million cell updates/sec

Title: US-09-651-685a-5

Perfect score: 114

Sequence: 1 CCYDASVNNDETCEORAR 20

Scoring table: BLOSUM62

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published_Applications_AA*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	114	100.0	20	9	US-09-878-603-5	Sequence 5, Appl
2	114	100.0	74	9	US-09-878-603-3	Sequence 3, Appl
3	111	97.4	20	9	US-09-878-603-68	Sequence 68, Appl
4	110	96.5	20	9	US-09-878-603-67	Sequence 67, Appl
5	110	96.5	20	9	US-09-878-603-69	Sequence 69, Appl
6	110	96.5	20	9	US-09-878-603-70	Sequence 70, Appl
7	110	96.5	20	9	US-09-878-603-71	Sequence 71, Appl
8	110	96.5	20	9	US-09-878-603-73	Sequence 73, Appl
9	109	95.6	19	9	US-09-878-603-54	Sequence 54, Appl
10	109	95.6	73	10	US-09-987-675-3	Sequence 3, Appl
11	109	95.6	1251	10	US-09-987-675-3	Sequence 3, Appl
12	109	95.6	1602	10	US-09-778-927A-58	Sequence 58, Appl
13	109	95.6	1602	10	US-09-778-927A-59	Sequence 59, Appl
14	108	94.7	20	9	US-09-878-603-64	Sequence 64, Appl
15	108	94.7	20	9	US-09-878-603-65	Sequence 65, Appl
16	106	93.0	20	9	US-09-878-603-72	Sequence 72, Appl
17	105	92.1	18	9	US-09-878-603-55	Sequence 55, Appl
18	105	92.1	19	9	US-09-878-603-59	Sequence 59, Appl
19	102	89.5	20	9	US-09-878-603-66	Sequence 66, Appl

20	101	88.6	17	9	US-09-878-603-56	Sequence 56, Appl
21	98	86.0	20	9	US-09-878-603-74	Sequence 74, Appl
22	96	84.2	16	9	US-09-878-603-57	Sequence 57, Appl
23	96	84.2	18	9	US-09-878-603-60	Sequence 60, Appl
24	94	82.5	74	9	US-09-878-603-7	Sequence 7, Appl
25	93	81.6	15	9	US-09-878-603-8	Sequence 8, Appl
26	91	79.8	15	9	US-09-878-603-58	Sequence 58, Appl
27	89	78.1	17	9	US-09-878-603-61	Sequence 61, Appl
28	85	74.6	354	9	US-10-039-050-2	Sequence 2, Appl
29	84	73.7	77	9	US-09-878-603-1	Sequence 1, Appl
30	83	72.8	16	9	US-09-878-603-62	Sequence 62, Appl
31	77	67.5	15	9	US-09-878-603-63	Sequence 63, Appl
32	51	44.7	20	9	US-09-878-603-2	Sequence 2, Appl
33	42	36.8	233	9	US-09-981-876-137	Sequence 137, App
34	42	36.8	233	9	US-09-148-545-137	Sequence 137, App
35	42	36.8	241	9	US-09-232-880-114	Sequence 114, App
36	42	36.8	241	9	US-10-012-896-114	Sequence 114, App
37	42	36.8	241	9	US-09-895-793-114	Sequence 114, App
38	42	36.8	241	9	US-09-895-814-114	Sequence 114, App
39	42	36.8	241	9	US-09-908-193-44	Sequence 44, App
40	42	36.8	241	10	US-09-759-143-114	Sequence 114, App
41	42	36.8	241	10	US-09-780-606-114	Sequence 114, App
42	42	36.8	241	10	US-09-030-606-114	Sequence 114, App
43	42	36.8	241	10	US-09-822-827-114	Sequence 114, App
44	42	36.8	241	10	US-09-115-453-114	Sequence 114, App
45	42	36.8	263	9	US-10-101-392-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-878-603-5
; Sequence 5, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: US-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; PRIOR FILING DATE: 2001-06-11
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-878-603-5

Query Match      100.0%; Score 114; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCYDASVNNDETCEORAR 20
Db      1 CCYDASVNNDETCEORAR 20

RESULT 2
US-09-878-603-3
; Sequence 3, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czermak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis

```

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FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 3
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-603-3

Query Match
Best Local Similarity 100.0%; Score 114; DB 9; Length 74;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCORAR 20
DB 21 CCYDGASVNNDETCORAR 40

RESULT 3
US-09-878-603-68
Sequence 68, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 68
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-68

Query Match
Best Local Similarity 97.4%; Score 111; DB 9; Length 20;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCORAR 20
DB 1 CCYDGATVNNDETCORAR 20

RESULT 4
US-09-878-603-67
Sequence 67, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
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SEQ ID NO 67
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-67

Query Match
Best Local Similarity 96.5%; Score 110; DB 9; Length 20;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCORAR 20
DB 1 CCYDGASVNNDESCORAR 20

RESULT 5
US-09-878-603-69
Sequence 69, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 69
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-69

Query Match
Best Local Similarity 95.0%; Score 110; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCORAR 20
DB 1 CCYDGASVNNDETCORAR 20

RESULT 6
US-09-878-603-70
Sequence 70, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 70
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-70

Query Match 96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||
DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 7
US-09-878-603-71

Sequence 71, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czermak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 71
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-71

Query Match 96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||
DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 8
US-09-878-603-73

Sequence 73, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czermak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 73
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-73

Query Match 96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
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DB 1 CCYDGASVNNDETCEQRAAR 20

RESULT 9
US-09-878-603-54
Sequence 54, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czermak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 54
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-54

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Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAA 19
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DB 1 CCYDGASVNNDETCEQRAA 19

RESULT 10
US-09-987-675-3
Sequence 3, Application US/09987675
Patent No. US20020169282A1
GENERAL INFORMATION:
APPLICANT: Canne, Lynne
APPLICANT: Kent, Stephen B.H.
TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
FILE REFERENCE: GREN-023/01US
CURRENT APPLICATION NUMBER: US/09/987,675
CURRENT FILING DATE: 2001-11-15
PRIOR FILING DATE: 1998-06-12
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 3
LENGTH: 73
TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-675-3

Query Match 95.6%; Score 109; DB 9; Length 73;
Best Local Similarity 95.0%; Pred. No. 4.7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
||||| |||||||
DB 20 CCYDGASVNNDETCEQRAAR 39

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RESULT 11
US-09-987-655-3
; Sequence 3, Application US/09987655
; Patent No. US20020132975A1
; GENERAL INFORMATION:
; APPLICANT: Canne, Lynne
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Simon, Reyna
; TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
; TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
; FILE REFERENCE: GREX-023/0105
; CURRENT APPLICATION NUMBER: US/09/987,655
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 09/097,094
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-655-3

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Query Match          95.6%; Score 109; DB 10; Length 73;
Best Local Similarity 95.0%; Pred. No. 4.7e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCYDGASVNNDETCEQRAAR 20
||||| ||||||| |||||
DB 20 CCYDGACVNNDETCEQRAAR 39

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RESULT 12
US-09-778-927A-58
; Sequence 58, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 58
; LENGTH: 1251
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1251)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-58

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Query Match          95.6%; Score 109; DB 10; Length 1251;
Best Local Similarity 95.0%; Pred. No. 8.6e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCYDGASVNNDETCEQRAAR 20
||||| ||||||| |||||
DB 698 CCYDGACVNNDETCEQRAAR 717

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RESULT 13
US-09-778-927A-59
; Sequence 59, Application US/09778927A

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; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 59
; LENGTH: 1602
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1602)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-59

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Query Match          95.6%; Score 109; DB 10; Length 1602;
Best Local Similarity 95.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCYDGASVNNDETCEQRAAR 20
||||| ||||||| |||||
DB 698 CCYDGACVNNDETCEQRAAR 717

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RESULT 14
US-09-878-603-64
; Sequence 64, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarna, Vidya
; APPLICANT: Czernek, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 64
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-64

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Query Match          94.7%; Score 108; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCYDGASVNNDETCEQRAAR 20
||||| ||||||| |||||
DB 1 CCYDGASVNNDETCEQRAAR 20

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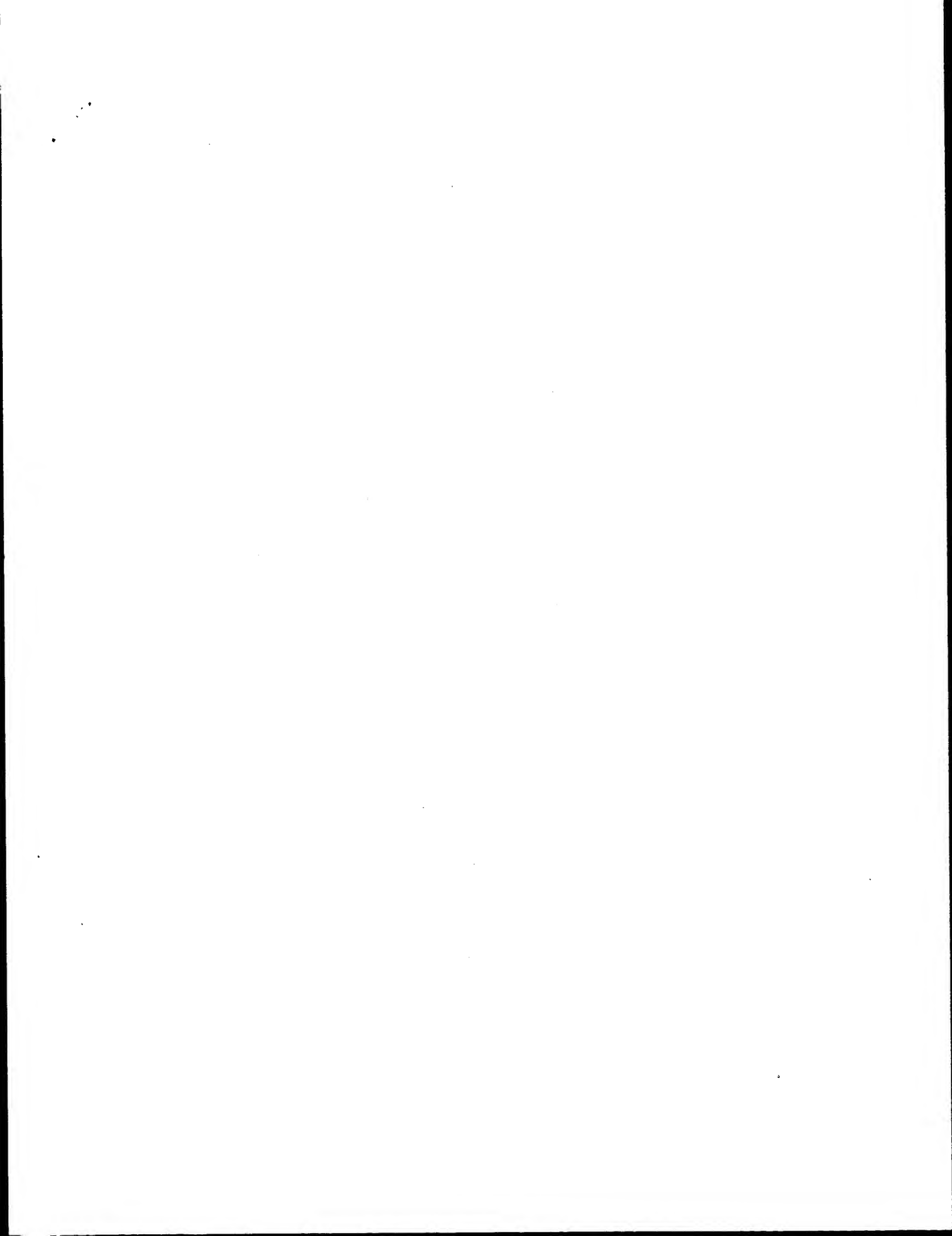
RESULT 15
US-09-878-603-65
; Sequence 65, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.

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APPLICANT: Huber-Lang, Markus
APPLICANT: Salma, Vidya
APPLICANT: Czermak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 65
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-65

Query Match 94.7%; Score 108; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.8e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCYDGASVNNDETCEORAR 20
DB 1 CCYDGASVNNDETCEORAR 20

Search completed: May 1, 2003, 22:24:49
Job time : 16 secs



GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:16:47 ; Search time 14 Seconds
(without alignments)
42.033 Million cell updates/sec

Title: US-09-651-685A-5
Sequence: 1 CCYDASVNDTCRORAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	95.6	73	4	US-09-097-094-3
2	109	95.6	74	1	US-08-463-224-3
3	109	95.6	74	2	US-08-463-377-3
4	109	95.6	74	4	US-09-246-500B-10
5	109	95.6	1676	4	US-08-487-283A-2
6	94	82.5	74	4	US-09-246-500B-12
7	93	81.6	74	4	US-09-246-500B-11
8	88	77.2	77	4	US-09-246-500B-14
9	84	73.7	77	4	US-09-246-500B-13
10	55.5	48.7	76	4	US-09-246-500B-8
11	51.5	45.2	77	4	US-09-246-500B-6
12	50.5	44.3	77	4	US-09-246-500B-7
13	48.5	42.5	76	4	US-09-246-500B-9
14	43.5	38.2	1651	1	US-08-447-411-2
15	42	36.8	71	2	US-08-972-008-4
16	42	36.8	71	4	US-09-267-409-4
17	42	36.8	241	3	US-08-808-148-1
18	42	36.8	241	4	US-09-020-956-114
19	42	36.8	241	4	US-09-030-607-114
20	42	36.8	241	4	US-09-605-785-114
21	42	36.8	241	4	US-09-439-313-114
22	42	36.8	241	4	US-09-352-616A-114
23	42	36.8	241	4	US-09-232-149A-114
24	42	36.8	263	2	US-08-972-008-2
25	42	36.8	263	4	US-09-141-027-2
26	42	36.8	263	4	US-09-267-409-2
27	41.5	36.4	1333	1	US-08-447-411-76

28	41.5	36.4	1333	2	US-08-662-227-34	Sequence 34, Appl
29	41.5	36.4	1333	4	US-09-017-947-34	Sequence 34, Appl
30	41	36.0	363	2	US-08-483-101-16	Sequence 16, Appl
31	40	35.1	751	2	US-08-836-443-3	Sequence 3, Appl
32	40	35.1	802	4	US-09-632-098-2	Sequence 2, Appl
33	40	35.1	812	4	US-09-632-098-4	Sequence 4, Appl
34	40	35.1	1940	2	US-08-644-271-30	Sequence 30, Appl
35	40	35.1	1940	4	US-09-077-955-34	Sequence 34, Appl
36	40	35.1	4544	1	US-08-469-486-52	Sequence 52, Appl
37	40	35.1	4544	2	US-08-469-658-52	Sequence 52, Appl
38	39.5	34.6	256	4	US-09-325-932A-57	Sequence 57, Appl
39	39	34.2	34	2	US-08-867-087B-64	Sequence 64, Appl
40	39	34.2	57	1	US-07-710-361-12	Sequence 12, Appl
41	39	34.2	217	1	US-07-697-275-2	Sequence 2, Appl
42	39	34.2	288	2	US-08-160-524A-6	Sequence 6, Appl
43	39	34.2	4654	4	US-08-476-515A-84	Sequence 84, Appl
44	39	34.2	4655	4	US-08-652-877-84	Sequence 84, Appl
45	39	34.2	4655	4	US-08-652-877-86	Sequence 86, Appl

ALIGNMENTS

```

RESULT 1
US-09-097-094-3
; Sequence 3, Application US/09097094
; Patent No. 6326468
; GENERAL INFORMATION:
; APPLICANT: Canne, Lynne
; APPLICANT: Kent, Stephen B. H.
; TITLE OF INVENTION: Solid Phase Native Chemical Ligation of Unprotected or
; TITLE OF INVENTION: N-Terminal Cysteine Protected Peptides in Aqueous
; FILE REFERENCE: GRN-023/01US
; CURRENT APPLICATION NUMBER: US/09/097, 094
; CURRENT FILING DATE: 1998-06-12
; EARLIER APPLICATION NUMBER: 60/049, 553
; EARLIER FILING DATE: 1997-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-097-094-3

Query Match          95.6%  Score 109;  DB 4;  Length 73;
Best Local Similarity 95.0%  Pred. No. 6.2e-10;
Matches 19;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      1  CCYDASVNDTCRORAR 20
DB      20  CCYDASVNDTCRORAR 39

RESULT 2
US-08-463-224-3
; Sequence 3, Application US/08463224
; Patent No. 5807824
; GENERAL INFORMATION:
; APPLICANT: van Oostrum, Jan
; APPLICANT: Boyar, William C.
; APPLICANT: Galakatos, Nicholas G.
; APPLICANT: Schmitz, Albert
; TITLE OF INVENTION: C5a Receptor Antagonists Having
; NUMBER OF SEQUENCES: 67
; SUBSTANTIALLY No. 5807824agonist Activity
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield

```

```

1 STATE: NJ
2 COUNTRY: USA
3 ZIP: 07090
4
5 COMPUTER READABLE FORM:
6
7 MEDIUM TYPE: Floppy disk
8
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0, Version #1.25
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/463,224
15 FILING DATE:
16
17 CLASSIFICATION: 435
18
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Rojew, Shawn P.
21
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: 908-654-5000
24 TELEFAX: 908-654-7866
25
26 TELEX: 139-125
27
28 INFORMATION FOR SEQ ID NO: 3:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 74 amino acids
31 TYPE: amino acid
32 TOPOLOGY: linear
33
34 MOLECULE TYPE: protein
35
36 US-08-463-224-3

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Query Match	95.68;	Score 109;	DB 1;	Length 74;
Best Local Similarity	95.08;	Pred. No. 6.3e-10;		
Matches 19;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

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Oy 1 CCYDGASVNNDETCEQRAAR 20
    ||||| ||||| |||||
Db 21 CCYDGACVNNDETCEQRAAR 40
```

RESULT 3
US-08-46

Sequence 3, Application US/08463377
Patent No. 5837499
GENERAL INFORMATION:
APPLICANT: van Oostrom, Jan
APPLICANT: Boyar, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: G5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5837499agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:

```

; ADDRESS: Lerner, David, Krumholz & Mentlik
; STREET: 600 South Avenue West
; CITY: Westfield
; STATE: NJ
; COUNTRY: US

```

STATE: NJ
COUNTRY: USA
STD: 07000

ZIP: 07090
COMPUTER READABLE FORM:
MEDICAL UNIT: 71-1111

COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS 3.31

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT ADDITIONAL DATA:

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CORRENT APPLICATION DATA:
APPLICATION NUMBER:  US/08/463,377
FILING DATE:

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CLASSIFICATION: 435

TELECOMMUNICATION INFORMATION:
NAME: Foley, Shawn P.
ATTORNEY/AGENCY INFORMATION:

TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866

TELEFAX: 308 634 / 8000
TELEX: 139-125
INFORMATION FOR SEO ID NO.:

SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids

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;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-463-377-3

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Query Match	95.6%	Score 109;	DB 2;	Length 74;
Best Local Similarity	95.0%;	Pred. No. 6.3e-10;		
Matches 19;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

```
QY 1 CCYDGASVNNDETCEÖRAAR 20
    ||||| ||||| |||||
Db 21 CCYDGACVNNDETCEÖRAAR 40
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RESULT 4
US-09-246-500B-10
; Sequence 10, Application US/09246500B

Patent NO. 6235494
GENERAL INFORMATION:

APPLICANT: HUGLI, TONY E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding Protein on Invention: Date of Invention: Date of Publication: 1981

```

; TITLE OF INVENTION:  Protein-Associated serine protease activity and methods
;
; TITLE OF INVENTION:  Using the Substrates
;
; PTE REFERENCE:  24720-2004

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; FILE REFERENCE: 24/30-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1000-03-08

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; CURREN1 FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0

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; SOFTWARE: FASTSEQ IOI WINDOWS VERSION 4.0
; SEQ ID NO 10
; LENGTH: 74

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' LENGTH: 7
; TYPE: PRT
: ORGANISM: Human [C5a Anaphylatoxin]

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NAME/KEY: CARBOHYD
FEATURE:
ORIGIN: human cca aaapnyraccaah

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LOCATION: (64) ... (66)
US-09-246-500B-10

Query Match	95.6%;	Score 109;	DB 4;	Length 74;
Best Local Similarity	95.0%;	Pred. No. 6.3e-10;		
Matches 19;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

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QY      1 CCYDGASVNNDETCEQRAR 20
          ||||| ||||| |||||
Db      21 CCYDGACVNNDETCEQRAR 40
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RESULT 5
US-08-487-283A-2

; Sequence 2, Application US/08487283A
; Patent No. 6355245

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; GENERAL INFORMATION:
; APPLICANT: Evans, Mark J.

```

APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen Elliott

APPLICANT: Nye, Steven H.
APPLICANT: Rollins, Scott

APPLICANT: Rother, Russell P.
APPLICANT: Springhorn, Jeremy P.

APPLICANT: Squinto, Stephen P.
APPLICANT: Thomas, Thomas C.

```

:      APPLICANT: Wilkins, James A.
:      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
:      OF OBESITY

```

TITLE OF INVENTION: OF INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 26

;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Seth A. Fidel
;
; CREDIT OF A

STREET: 25 Science
CITY: New Haven

STATE: CONNECTICUT
COUNTRY: USA
STD: 06511

```

; ZIP: 00511
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5 inch 1 amb storage

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COMPUTER: Macintosh Cetrus 610
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,208
FILING DATE: 02-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seth A. Fidel.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)776-1790
TELEFAX: (203)772-3655
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1676 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE:
DESCRIPTION: Pro-C5 Polypeptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Haviland, D.L.
AUTHORS: Haviland, J.C.
AUTHORS: Fleischer, D.T.
AUTHORS: Hunt, A.
AUTHORS: Wetsel, R.A.
TITLE: Complete cDNA Sequence of Human
Patent No. 6355245
TITLE: Complement Pro-C5
JOURNAL: Journal of Immunology
VOLUME: 146
PAGES: 362-368
DATE: 1991
US-08-487-283A-2

Query Match 95.6%; Score 109; DB 4; Length 1676;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 698 CCYDGACVNNDETCEORAR 717

RESULT 6
US-09-246-500B-12
Sequence 12 Application US/09246500B
Patent No. 6235494
GENERAL INFORMATION:
APPLICANT: Hugill, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
FILE REFERENCE: 24730-2204
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 12
LENGTH: 74
TYPE: PRT
ORGANISM: Cow C5a Anaphylatoxin
US-09-246-500B-12

Query Match 82.5%; Score 94; DB 4; Length 74;

Best Local Similarity 80.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 21 CCYDGARVNNDETCEORAR 40

RESULT 7
US-09-246-500B-11
Sequence 11 Application US/09246500B
Patent No. 6235494
GENERAL INFORMATION:
APPLICANT: Hugill, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
FILE REFERENCE: 24730-2204
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 11
LENGTH: 74
TYPE: PRT
ORGANISM: Pig C5a Anaphylatoxin
FEATURE:
NAME/KEY: CARBOHYD
LOCATION: (64)...(66)
US-09-246-500B-11

Query Match 81.6%; Score 93; DB 4; Length 74;
Best Local Similarity 80.0%; Pred. No. 1.8e-07;
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 21 CCYDGARVNNDETCEORAR 40

RESULT 8
US-09-246-500B-14
Sequence 14 Application US/09246500B
Patent No. 6235494
GENERAL INFORMATION:
APPLICANT: Hugill, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
FILE REFERENCE: 24730-2204
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 14
LENGTH: 77
TYPE: PRT
ORGANISM: Mouse C5a Anaphylatoxin
US-09-246-500B-14

Query Match 77.2%; Score 88; DB 4; Length 77;
Best Local Similarity 80.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 24 CCYDGARVNNDETCEORAR 43

RESULT 9
US-09-246-500B-13
Sequence 13 Application US/09246500B
Patent No. 6235494

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; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Rat C5a Anaphylatoxin
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (67)...(69)
US-09-246-500B-13

Query Match          73.7%; Score 84; DB 4; Length 77;
Best Local Similarity 75.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 CCYDASVNNDETCEORAR 20
        ||||| | ||||| |
Db      24 CCYDGAENKYECEORVAR 43

RESULT 10
US-09-246-500B-8
; Sequence 8, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Rat C4a Anaphylatoxin
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (66)...(68)
US-09-246-500B-8

Query Match          48.7%; Score 55.5; DB 4; Length 76;
Best Local Similarity 57.1%; Pred. No. 0.099;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

QY      1 CCYDGA-ASVNNDETCEORAR 20
        || | | : ||||| |
Db      23 CCQDGMTRLPMTARCEORAR 43

RESULT 11
US-09-246-500B-6
; Sequence 6, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Mouse C4a Anaphylatoxin
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (66)...(68)
US-09-246-500B-9

Query Match          42.5%; Score 48.5; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Human C4a Anaphylatoxin
US-09-246-500B-6

Query Match          45.2%; Score 51.5; DB 4; Length 77;
Best Local Similarity 52.4%; Pred. No. 0.41;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY      1 CCYDGA-ASVNNDETCEORAR 20
        || | | : ||||| |
Db      23 CCQDGMTRLPMTARCEORAR 43

RESULT 12
US-09-246-500B-7
; Sequence 7, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Cow C4a Anaphylatoxin
US-09-246-500B-7

Query Match          44.3%; Score 50.5; DB 4; Length 77;
Best Local Similarity 52.4%; Pred. No. 0.59;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY      1 CCYDGA-ASVNNDETCEORAR 20
        || | | : ||||| |
Db      23 CCQDGMTRLPMTARCEORAR 43

RESULT 13
US-09-246-500B-9
; Sequence 9, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 9
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Mouse C4a Anaphylatoxin
; FEATURE:
; NAME/KEY: CARBOHYD
; LOCATION: (66)...(68)
US-09-246-500B-9

Query Match          42.5%; Score 48.5; DB 4; Length 76;
Best Local Similarity 50.0%; Pred. No. 1.2;
Matches 10; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
```

Db 23 CCODGVTRLPMKRSCEQRAA 42

RESULT 14
US-08-447-411-2

Sequence 2, Application US/08447411

Patent No. 5773243

GENERAL INFORMATION:

APPLICANT: FRITZINGER, DAVID C.

APPLICANT: BREDEHORST, REINHARD

APPLICANT: VOGEL, CARL-WILHELM

TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/447,411

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/043,747

FILING DATE: 07-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NO. 5773243man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 1126-101-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1651 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-447-411-2

Query Match

Best Local Similarity 38.2%; Score 43.5; DB 1; Length 1651;

Matches 10; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

Db 683 CCODGVTRLPMKRSCEQRAA 701

RESULT 15

US-08-972-008-4

Sequence 4, Application US/08972008

Patent No. 5942420

GENERAL INFORMATION:

APPLICANT: HOLTZMAN, Douglas A.

TITLE OF INVENTION: No. 5942420el Molecules of the Follistatin-Related

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/972,008

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragoras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: MNT-026

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-4214

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 71 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-972-008-4

Query Match

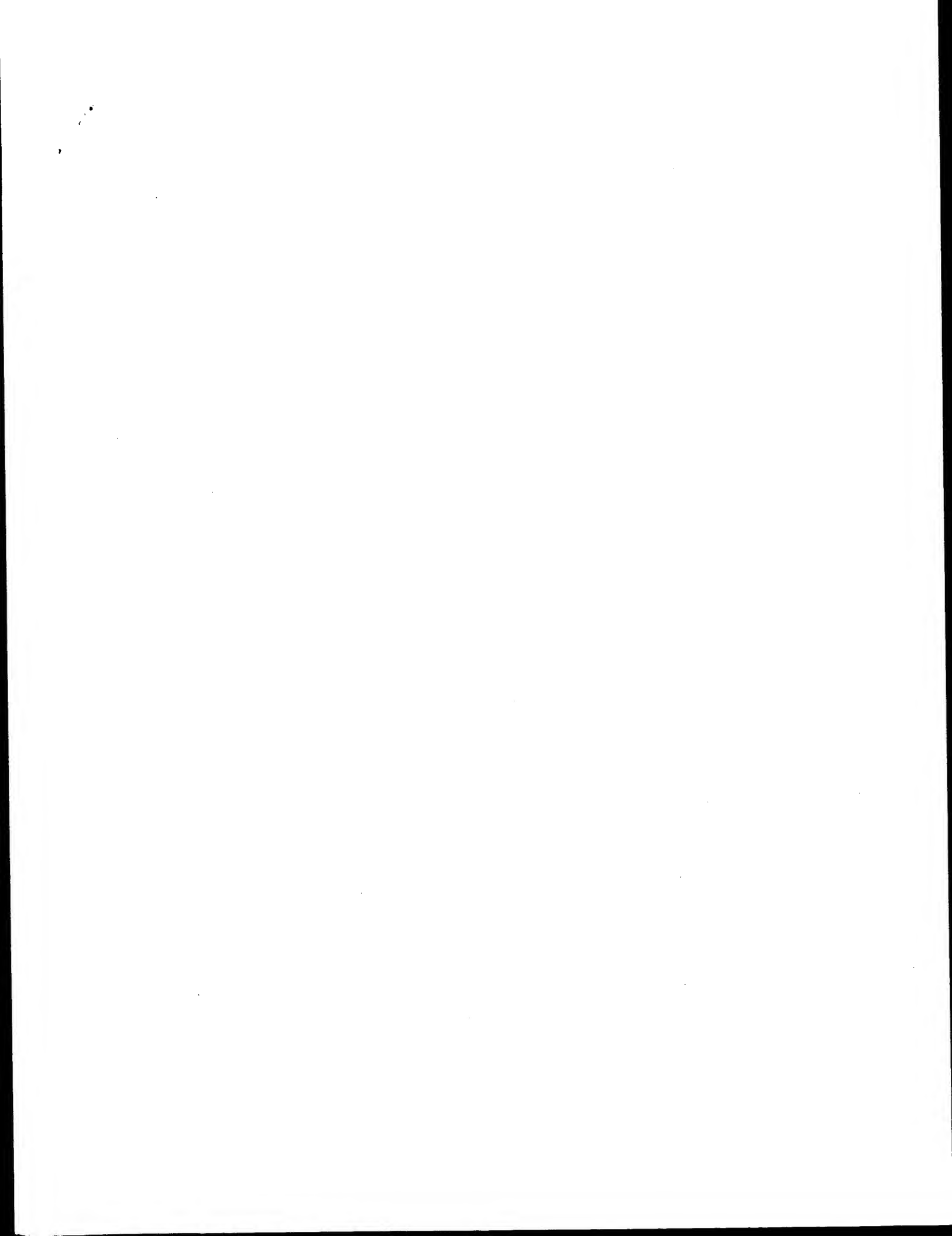
Best Local Similarity 36.8%; Score 42; DB 2; Length 71;

Matches 10; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Db 39 CGSDGATYRDE--CELRAAR 56

Search completed: May 1, 2003, 22:20:26

Job time: 15 secs



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:24:32 ; Search time 15 Seconds
(without alignments)
128.179 Million cell updates/sec

Title: US-09-651-685a-5
Sequence: 1 CCYDASVNDCTCQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.5	27.6	16	2 A59042	alpha-conotoxin Epi
2	29.5	25.9	18	1 A58589	alpha-conotoxin Epi
3	28	24.6	20	2 B44907	manganese peroxidase
4	26	22.8	13	1 NTKNAS	alpha-conotoxin SI
5	25	21.9	16	2 A59045	alpha-conotoxin Au
6	25	21.9	16	2 A54877	alpha-conotoxin pn
7	25	21.9	18	1 QHEC2	heat-stable entero
8	25	21.9	20	2 PC2248	lambda 112 protein
9	24	21.1	14	2 A48389	lelutoxin III -
10	24	21.1	16	2 PD0002	inulin fructotrans
11	23	20.2	12	2 S28215	glucan endo-1,3-be
12	23	20.2	14	1 NTKNIM	alpha-conotoxin MI
13	23	20.2	16	2 S60171	sex-lethal protein
14	23	20.2	17	2 S60171	plasma membrane ca
15	23	20.2	18	2 D49570	T-cell receptor be
16	23	20.2	19	2 B48839	trypanin inhibitor
17	23	20.2	18	2 PS0236	equilibrin 1B - s
18	23	20.2	20	2 PC1150	equilibrin 1B - s
19	22	19.3	12	1 A53709	alpha-conotoxin Im
20	22	19.3	13	2 A60379	factor X activator
21	22	19.3	19	2 PH1330	Ig heavy chain DJ
22	22	19.3	20	2 S08605	hypothetical prote
23	22	19.3	20	2 H49164	chromogranin-B - r
24	22	19.3	20	2 H49164	lectin, galactose/
25	21.5	18.9	13	2 B58533	CD61 homolog - cha
26	21	18.4	10	2 PC4442	cytochrome c553 -
27	21	18.4	11	2 D45900	complement C3b rec
28	21	18.4	15	2 S49409	H+-transporting tw
29	21	18.4	15	2 PH1318	Ig heavy chain DJ

30	21	18.4	16	2 C59045	alpha-conotoxin Au
31	21	18.4	16	2 B54877	alpha-conotoxin pn
32	21	18.4	16	2 H49039	T-cell receptor be
33	21	18.4	16	2 PL0137	protein kinase, 80
34	21	18.4	16	4 I79565	hypothetical rctL3/
35	21	18.4	17	2 I58087	ryanodine receptor
36	21	18.4	18	2 J00125	polypheuslin II -
37	21	18.4	19	2 C21182	4K prothoracicopro
38	21	18.4	19	2 A21182	4K prothoracicopro
39	21	18.4	19	2 A49254	TCR delta chain V-
40	21	18.4	19	2 S65435	manganese peroxidase
41	21	18.4	20	2 JT0410	bombyxin-IV chain
42	21	18.4	20	2 D25507	protease inhibitor
43	21	18.4	20	2 S48746	beta tubulin b-bet
44	20	17.5	8	2 D61512	variant surface gl
45	20	17.5	11	2 S65395	chemical-sense-rel

ALIGNMENTS

RESULT 1

A59042
alpha-conotoxin Epi - cone shell (Conus episcopatus)
C:Species: Conus episcopatus (bishop's cone)
C:Date: 23-Jul-1999 #sequence #revision 23-Jul-1999 #text_change 13-Aug-1999
C:Accession: A59042
R: Loughman, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, J. Biol. Chem. 273, 15667-15674, 1998
A:Title: Alpha-conotoxin Epi, a novel sulfated peptide from Conus episcopatus that se
A:Reference number: A59042; MUID:98288307; PMID:9624161
A:Accession: A59042
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-16 <CD>
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
F:1-16/Product: alpha-conotoxin Epi #status experimental <MAT>
F:2-8,3-16/Disulfide bonds: #status experimental
F:15/Binding site: sulfated (Tyr) (covalent) #status experimental
F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 27.6%; Score 31.5; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
QY 1 CCYD-GASVNDCTC 14
DB 2 CCSDPRCMNNDPDC 16

RESULT 2

A58589
alpha-conotoxin Epi - cone shell (Conus ermineus)
C:Species: Conus ermineus (ermine cone)
C:Date: 10-Sep-1999 #sequence #revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A58589
R: Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N
Biochemistry 34, 14519-14526, 1995
A:Title: alpha-Conotoxin Epi, a new nicotinic acetylcholine receptor antagonist with n
A:Reference number: A58589; MUID:96062516; PMID:7578057
A:Accession: A58589
A:Molecule type: protein
A:Residues: 1-18 <MAR>
A:Note: sequence confirmed by chemical synthesis
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline;
F:3/Modified site: 4-hydroxyproline (Pro) #status experimental
F:4-10,5-18/Disulfide bonds: #status experimental
F:18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match

25.9%; Score 29.5; DB 1; Length 18;

Best Local Similarity 33.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 CCYDASVNDNDC 14
||| : : :
Db 4 CCHPACGKKNPD 18

RESULT 3

B44907 manganese peroxidase (EC 1.11.1.13) H3 - basidiomycete (Phanerochaete chrysosporium) (fr

C:Species: Phanerochaete chrysosporium
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 06-Dec-1996
C:Accession: B44907

R:Pease, E.A.; Tien, M.

J. Bacteriol. 174, 3532-3540, 1992

A:Title: Heterogeneity and regulation of manganese peroxidases from Phanerochaete chrysosporium

A:Reference number: A44907; PMID:1592808

A:Accession: B44907

A:Molecule type: protein

A:Residues: 1-20 <PEA>

A:Experimental source: BKM-F-1767, ATCC 24725

A:Note: sequence extracted from NCBI backbone (NCBI:104607)

C:Superfamily: lignin peroxidase

C:Keywords: extracellular protein; glycoprotein; heme; oxidoreductase

Query Match 24.6%; Score 28; DB 2; Length 20;

Best Local Similarity 71.4%; Pred. No. 7.3e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 DGASVNN 10
||| : : :
Db 5 DGTGVNN 11

RESULT 4

NTKNS alpha-conotoxin SIA - cone shell (Conus striatus)

C:Species: Conus striatus (striated cone)

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-May-1997

C:Accession: A40312

R:Myers, R.A.; Zafaralla, G.C.; Gray, W.R.; Abbott, J.; Cruz, L.J.; Olivera, B.M.

Biochemistry 30, 9370-9377, 1991

A:Title: alpha-Conotoxins, small peptide probes of nicotinic acetylcholine receptors.

A:Reference number: A40312; PMID:1892838

A:Accession: A40312

A:Molecule type: protein

A:Residues: 1-13 <MYE>

C:Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neurot

F:2-7,3-13/Disulfide bonds: #status experimental

F:13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 22.8%; Score 26; DB 1; Length 13;

Best Local Similarity 36.4%; Pred. No. 9.8e+02;

Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CCYDASVNNND 11
||| : : :
Db 2 CCHPACGKKNPD 12

RESULT 5

A59045 alpha-conotoxin AUIA - cone shell (Conus aulicus)

C:Species: Conus aulicus (cone cone)

C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: A59045

R:Luo, S.; Tjalk, J.M.; Gattler, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McI

J. Neurosci. 18, 8571-8579, 1998

A:Title: Alpha-conotoxin AUIA selectively blocks alpha3beta4 nicotinic acetylcholine rec

A:Reference number: A59045; PMID:99003392; PMID:9786965

A:Accession: A59045
A:Status: preliminary
A:Molecule type: protein

A:Residues: 1-16 <LUO>

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:1-16/Product: alpha-conotoxin AUIA #status experimental <MAT>

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 21.9%; Score 25; DB 2; Length 16;

Best Local Similarity 28.6%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCYDASVNNDC 14
||| : : :
Db 3 CSTPPCFATNSDYC 16

RESULT 6

A54877 alpha-conotoxin PNIA [validated] - cone shell (Conus pennaceus)

N:Alternate names: alpha-CTX-PNIA

C:Species: Conus pennaceus

C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Sep-2000

C:Accession: A54877

R:Palzniber, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.E.; Zl

Biochemistry 33, 9523-9529, 1994

A:Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine r

A:Reference number: A54877; PMID:94347719; PMID:8068627

A:Accession: A54877

A:Molecule type: protein

A:Residues: 1-16 <FAI>

R:Hu, S.H.; Gehrmann, J.; Guddat, L.W.; Alewood, P.F.; Craik, D.J.; Martin, J.L.

submitted to the Brookhaven Protein Data Bank, January 1996

A:Reference number: A66355; PDB:1PEN

A:Contents: annotation; X-ray crystallography, 1.1 angstroms; residues 1-16

C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn

C:Superfamily: alpha-conotoxin

C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu

F:2-8,3-16/Disulfide bonds: #status experimental

F:16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 21.9%; Score 25; DB 2; Length 16;

Best Local Similarity 28.6%; Pred. No. 1.7e+03;

Matches 4; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCYDASVNNDC 14
||| : : :
Db 3 CSTPPCAANNPDYC 16

RESULT 7

QHEC2

heat-stable enterotoxin ST-2 - Escherichia coli

C:Species: Escherichia coli

C:Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 31-Dec-1996

C:Accession: A01823

R:Chan, S.K.; Giannelis, R.A.

J. Biol. Chem. 256, 7744-7746, 1981

A:Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli

A:Reference number: A01823; PMID:81264141; PMID:7021541

A:Accession: A01823

A:Molecule type: protein

A:Residues: 1-18 <CHA>

A:Experimental source: strain 18D, serotype 0.42:H6:H37

C:Comment: This enterotoxin is one of several, of differing molecular sizes, produced

ides of the heat-stable enterotoxin ST-1.

C:Superfamily: heat-stable enterotoxin ST

C:Keywords: enterotoxin; heat-stable protein

F:1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>

F:5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match
Best Local Similarity 21.9%; Score 25; DB 1; Length 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCY 3
DB 9 CCY 11

RESULT 8

PC2248
lambda 112 protein - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 17-Sep-1997
C:Accession: PC2248
R:Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.; Yanagihara, I.; Iseigawa, Biochem. Biophys. Res. Commun. 198, 485-491, 1994
A:Title: Krabbe disease: Isolation and characterization of a full-length cDNA for human
A:Reference number: J02397; MUID:94128088; PMID:8297359
A:Accession: PC2248
A:Molecule type: mRNA
A:Residues: 1-20 <SAK>
A:Cross-references: DDBJ:D25284

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCY 3
DB 5 CCY 7

RESULT 9

A48389
lelurutoxin III - Egyptian scorpion (fragment)

C:Species: Leiurus quinquestriatus (Egyptian scorpion)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A48389
R:Valdavid, H.H.; Martin, B.M.; Escobar, L.; Possani, L.D.
Biochem. Int. 27, 953-962, 1992
A:Title: Noxustoxin and lelurutoxin III, two homologous peptide toxins with binding pro
A:Reference number: A48389; MUID:93075256; PMID:1280139
A:Accession: A48389
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <VAL>
A:Experimental source: venom
A:Note: sequence extracted from NCBI backbone (NCBIP:117118)

Query Match
Best Local Similarity 21.1%; Score 24; DB 2; Length 14;
Matches 5; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

OY 2 CYDGASVNDDECE 15
DB 7 CYDSSQ-----CE 14

RESULT 10

PD0002
Inulin fructotransferase (depolymerizing, difructofuranose-1,2'-2,3'-dianhydride-forming

C:Species: Bacillus sp.
C:Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 03-Jun-2002
C:Accession: PD0002
R:Kang, S.I.; Kim, W.P.; Chang, Y.J.; Kim, S.I.
Bioosci. Biotechnol. Biochem. 62, 628-631, 1998
A:Title: Purification and properties of inulin fructotransferase (DFA III-producing) fr
A:Reference number: PD0002
A:Accession: PD0002
A:Molecule type: protein
A:Residues: 1-16 <KAN>
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match
Best Local Similarity 21.1%; Score 24; DB 2; Length 16;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 DGASVNDDET 13
DB 5 DGAPLVQVNT 14

RESULT 11

S28215
glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) GII - barley (fragment)
N:Alternate names: (1-3)-beta-D-glucanase GII
C:Species: Hordeum vulgare (barley)
C:Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 07-May-1999
C:Accession: S28215
R:Hrmova, M.; Fincher, G.B.
Biochem. J. 289, 453-461, 1993
A:Title: Purification and properties of three (1->3)-beta-D-glucanase isoenzymes from
A:Reference number: S28214; MUID:93143715; PMID:8424790
A:Accession: S28215
A:Molecule type: protein
A:Residues: 1-12 <HRM>
A:Experimental source: cultivar Clipper
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match
Best Local Similarity 20.2%; Score 23; DB 2; Length 12;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CYDGASVN 9
DB 4 CYGGIGNN 11

RESULT 12

NTK1NM
alpha-conotoxin MI - cone shell (Conus magus)
C:Species: Conus magus (magus cone)
C:Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 16-Jul-1999
C:Accession: A01784
R:McIntosh, M.; Cruz, L.J.; Hunnkapiller, M.W.; Gray, W.R.; Olivera, B.M.
Arch. Biochem. Biophys. 218, 329-334, 1982
A:Title: Isolation and structure of a peptide toxin from the marine snail Conus magus
A:Reference number: A90071; MUID:83073458; PMID:7149738
A:Accession: A01784
A:Molecule type: protein
A:Residues: 1-14 <MCIS>

R:Gray, W.R.; Rivier, J.E.; Galyean, R.; Cruz, L.J.; Olivera, B.M.
J. Biol. Chem. 258, 12247-12251, 1983
A:Title: Conotoxin MI. Disulfide bonding and conformational states.
A:Reference number: A92396; MUID:84032400; PMID:6630187
A:Contents: annotation; disulfide bonds
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
E:3-B,4-14/Disulfide bonds: #status experimental
E:14/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match
Best Local Similarity 20.2%; Score 23; DB 1; Length 14;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 CCYDGASVN 9
DB 3 CCHPACGKN 11

RESULT 13

PH1317
Ig heavy chain DJ region (clone C527-112) - human (fragment)
C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1317
 R:Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A>Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A:Reference number: PH1302; MIMD:93094761; PMID:1460419
 A:Accession: PH1317
 A:Molecule type: DNA
 A:Residues: 1-16 <WAS>
 C:Keywords: heterotetramer; immunoglobulin

Query Match 20.2%; Score 23; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 CYDGAS 7
 11 11:
 Db 5 CYGGS 10

RESULT 14

S60171
 sex-lethal protein - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 17-Mar-1999
 C:Accession: S60171
 R:Hoshijima, K.; Kohyama, A.; Watakabe, I.; Inoue, K.; Sakamoto, H.; Shimura, Y.
 Nucleic Acids Res. 23, 3441-3448, 1995
 A>Title: Transcriptional regulation of the Sex-lethal gene by helix-loop-helix proteins.
 A:Reference number: S60171; MIMD:96032836; PMID:7567454
 A:Accession: S60171
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-17 <HOS>
 A:Cross-references: EMBL:D50435
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
 C:Genetics:
 A:Gene: FlyBase:Sc1
 A:Cross-references: FlyBase:FBgn0003659

Query Match 20.2%; Score 23; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 3.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 13 TCEORA 18
 11 11:
 Db 12 TCYORS 17

RESULT 15

D49570
 plasma membrane calcium pump - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 12-Dec-1997
 C:Accession: D49570
 R:Stauffer, T.P.; Hilfinger, H.; Carafoli, E.; Strehler, E.E.
 J. Biol. Chem. 268, 25993-26003, 1993
 A>Title: Quantitative analysis of alternative splicing options of human plasma membrane
 A:Reference number: A49570; MIMD:94064681; PMID:8245032
 A:Accession: D49570
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-18 <STRA>
 A:Experimental source: cerebral cortex
 A>Note: sequence inconsistent with nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBIN:139934, NCBI:P:139939)
 C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C:Keywords: ATP

Query Match 20.2%; Score 23; DB 2; Length 18;
 Best Local Similarity 75.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 CYDG 5
 11 11:
 Db 5 CWDG 8

Search completed: May 1, 2003, 22:27:40
 Job time: 17 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:20:32 ; Search time 25 Seconds

(without alignments)
33.181 Million cell updates/sec

Title: US-09-651-685a-5
Perfect score: 114
Sequence: 1 CCYDGSVNNDETCGRAR 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 1147

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.5	27.6	16	1	CXAL_CONEP
2	29.5	25.9	18	1	CXAL_CONEP
3	29	25.4	15	1	ITRB_ALBU
4	26	22.8	13	1	CXAA_CONST
5	25	21.9	16	1	CXAL_CONEP
6	25	21.9	16	1	CXAA_CONEP
7	25	21.9	18	1	HSTR_ECOLI
8	25	21.9	19	1	LCRP_PETMA
9	24	21.1	14	1	SCRP_LEIOU
10	24	20.2	14	1	SB60_MAIZE
11	23	20.1	20	1	CXAL_CONEP
12	22	19.3	12	1	CXAL_CONEP
13	21	18.4	15	1	UNO1_PINPS
14	21	18.4	16	1	CXAB_CONEP
15	21	18.4	18	1	PWM2_LIMO
16	21	18.4	20	1	SC18_MESMA
17	21	18.4	20	1	RRPL_PHODV
18	20	17.5	10	1	CX5A_CONEP
19	20	17.5	11	1	CX5B_CONEP
20	20	17.5	13	1	CX1A_CONEP
21	20	17.5	14	1	CX1B_CONEP
22	20	17.5	15	1	CX1B_CONEP
23	20	17.5	15	1	CX1B_CONEP
24	20	17.5	15	1	CX1B_CONEP
25	20	17.5	15	1	CX1B_CONEP
26	20	17.5	15	1	CX1B_CONEP
27	20	17.5	15	1	CX1B_CONEP
28	20	17.5	15	1	CX1B_CONEP
29	20	17.5	15	1	CX1B_CONEP
30	20	17.5	15	1	CX1B_CONEP
31	20	17.5	15	1	CX1B_CONEP
32	20	17.5	15	1	CX1B_CONEP
33	20	17.5	15	1	CX1B_CONEP

34	19	16.7	10	1	COXA_ONCMY
35	19	16.7	10	1	PPCK_FASHE
36	19	16.7	10	1	UH05_RAT
37	19	16.7	15	1	GUAN_DIDMA
38	19	16.7	16	1	ARCD_PSEPU
39	19	16.7	17	1	CXMA_CONEP
40	19	16.7	17	1	CXMA_CONEP
41	19	16.7	17	1	CXMA_CONEP
42	19	16.7	18	1	PATS_ANASP
43	19	16.7	18	1	UC03_MAIZE
44	19	16.7	19	1	FTBB_TAPTE
45	19	16.7	19	1	HMD_METWO

ALIGNMENTS

RESULT 1	
CXAL_CONEP	STANDARD; PRT; 16 AA.
ID	CXAL_CONEP
AC	P5638;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Alpha-conotoxin Epi.
OS	Conus episcopatus (Bishop's cone).
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC	Neogastropoda; Conoidea; Conidae; Conus.
ON	NCBI_TaxID=88764;
RX	X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RA	MEDLINE=98376423; PubMed=9708977;
RA	Hu S.H., Loughnan M., Miller R., Weeks C.M., Blessing R.H.,
RT	Alewood P.F., Lewis R.J., Martin J.L.;
RT	"The 1.1-A resolution crystal structure of [Tyr15]Epi, a novel
RL	alpha-conotoxin from Conus episcopatus, solved by direct methods."
CC	Biochemistry 37:11425-11433(1998).
CC	-1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC	BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC	INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
CC	ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-2 AND ALPHA-
CC	3/BETA-4 SUBUNITS.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC	-1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
DR	PDB: 1A0M, 13-JAN-99.
KW	postsynaptic neurotoxin; Neurotoxin; Toxin;
KW	Acetylcholine receptor inhibitor; Amidation;
FT	Sulfation; 3D-structure.
FT	DISULFID 2
FT	MOD.RES 3 16
FT	MOD.RES 15 15
FT	MOD.RES 16 16
SO	SEQUENCE 16 AA; 1792 MW; C63385F376C99B4C CRC64;
QY	Query Match 27.6%; Score 31.5; DB 1; Length 16;
QY	Best local Similarity 40.0%; Pred. No. 48;
QY	Matches 6; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
DB	2 CCSDPRCANNPDYC 16
RESULT 2	
CXAL_CONEP	STANDARD; PRT; 18 AA.
ID	CXAL_CONEP
AC	P50982;
DT	01-OCT-1996 (Rel. 34, Created)
DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Alpha-conotoxin Epi.

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OS Conus ermineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;

RN
  (1)
  SEQUENCE.
  RP TISSUE=Venom;
  RC MEDLINE=96062516; PubMed=7578057;
  RA Martinez J.S., Olivera B.M., Gray W.R., Craig A.G., Groebe D.R.,
  RA Abramson S.N., McIntosh J.M.;
  RT "Alpha-conotoxin R1, a new nicotinic acetylcholine receptor
  RT antagonist with novel selectivity.";
  RL Biochemistry 34:14519-14526(1995).
  CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
  CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
  CC INHIBIT THEM.
  CC -1- SUBUNIT: Binds nicotinic acetylcholine receptor.
  CC -1- SUBCELLULAR LOCATION: Secreted.
  CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
  CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
  CC FAMILY.
  CC Postsynaptic neurotoxin; Neurotoxin; Toxin;
  KW Acetylcholine receptor inhibitor; Amidation; Hydroxylation.
  FT DISULFID 4 10
  FT DISULFID 5 18
  FT MOD_RES 3 3
  FT MOD_RES 18 18
  FT MOD_RES 18 18
  FT SEQUENCE 18 AA; 2082 MW; 60A61AC427A6B5E CRC64;

OY Query Match 25.9%; Score 29.5; DB 1; Length 18;
  Best local Similarity 33.3%; Pred. No. 1.1e+02;
  Matches 5; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

DB 4 CCYHPGMSNPQIC 18

RESULT 3
ITRB ALBU
ID ITRB ALBU STANDARD; PRT; 15 AA.
AC P24927;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Trypsin inhibitor B chain (Fragment).
DE Albizia julibrissin (Silk tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizia.
OX NCBI_TaxID=3813;
RN
  (1)
  SEQUENCE.
  RP TISSUE=Seed;
  RC MEDLINE=80115605; PubMed=528539;
  RA Odani S., Ono T., Ikenaka T.;
  RT "Proteinase inhibitors from a mimosoideae legume, Albizia
  RT julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
  RL J. Biochem. 86:1795-1805(1979).
  CC -1- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
  CC -1- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A
  CC DISULFIDE BOND.
  CC -1- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
  CC FAMILY.
  CC Serine protease inhibitor.
  KW NON_TER 15
  FT NON_TER 15
  FT SEQUENCE 15 AA; 1705 MW; 53165F7E9C45B4D0 CRC64;

OY Query Match 25.4%; Score 29; DB 1; Length 15;
  Best local Similarity 45.5%; Pred. No. 1.1e+02;
  Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 2 CCYDASVNNDE 12

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DB 5 CKDGSIDDE 15

RESULT 4
CXAL_CONSL
ID CXAL_CONSL STANDARD; PRT; 13 AA.
AC P28678;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin SIA (SIA).
DE Alpha-conotoxin SIA (SIA).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN
  (1)
  SEQUENCE.
  RP TISSUE=Venom;
  RC MEDLINE=91369955; PubMed=1892838;
  RA Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
  RA Olivera B.M.;
  RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
  RT receptors.";
  RL Biochemistry 30:9370-9377(1991).
  CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
  CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
  CC INHIBIT THEM.
  CC -1- SUBCELLULAR LOCATION: Secreted.
  CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
  CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
  CC FAMILY.
  CC PIR: A40312; NTKNAS.
  KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
  KW Acetylcholine receptor inhibitor; Amidation.
  FT DISULFID 2 7
  FT DISULFID 3 13
  FT MOD_RES 13 13
  FT MOD_RES 13 13
  FT SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

OY Query Match 22.8%; Score 26; DB 1; Length 13;
  Best local Similarity 36.4%; Pred. No. 2.9e+02;
  Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

DB 2 CCHPACGKNPD 12

RESULT 5
CXAL_CONSL
ID CXAL_CONSL STANDARD; PRT; 16 AA.
AC P56639;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin AUIA.
DE Alpha-conotoxin AUIA.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;
RN
  (1)
  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
  RP TISSUE=Venom;
  RC MEDLINE=99003392; PubMed=9786965;
  RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
  RA Olivera B.M., McIntosh J.M.;
  RT "Alpha-conotoxin AUIB selectively blocks alpha3 beta4 nicotinic
  RT acetylcholine receptors and nicotine-evoked norepinephrine release.";
  RL J. Neurosci. 18:8571-8579(1998).
  CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
  CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
  CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC

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CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE FAMILY.
 DR HSP: P50984; 1PEN.
 KM Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KM Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA: 1731 MW: 1E310FB8FDC7001 CRC64;
 Query Match 21.9%; Score 25; DB 1; Length 16;
 Best Local Similarity 28.6%; Pred. No. 5.1e+02;
 Matches 4; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCYDASVNNDET 14
 DB 3 CSYPCFATNSDYC 16

RESULT 6
 ID CXXA_CONPE STANDARD; PRT: 16 AA.
 AC P50984;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Pn1a.
 OS Conus pennaceus (Feathered cone).
 OC Eukaryota; Metazoa; Mollusca; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=94347719; PubMed=8068627;
 RA Fainzilber M., Hesson A., Oren R., Burlingame A.L., Gordon D.,
 RA Spira M.E., Zlotkin E.;
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors.";
 RL Biochemistry 33:9523-9529(1994).
 RN [2]
 RP Sulfation of Tyr-15.
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-Pn1a and alpha-Pn1B: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry.";
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RX MEDLINE=96311277; PubMed=8740364;
 RA Hu S.-H., Gehrmann J., Guedat L.W., Alewood P.F., Craik D.J.,
 RA Martin J.L.;
 RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor
 RT antagonist, alpha-conotoxin Pn1a from Conus pennaceus.";
 RL Structure 4:417-423(1996).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES. THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
 CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
 CC PENNACEUS ALPHA-CONOTOXINS SECRETED.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1PEN; 21-APR-97.

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KM Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 SQ SEQUENCE 16 AA: 1628 MW: 03310FF93EC99005 CRC64;
 Query Match 21.9%; Score 25; DB 1; Length 16;
 Best Local Similarity 28.6%; Pred. No. 5.1e+02;
 Matches 4; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 CCYDASVNNDET 14
 DB 3 CSUPECAANNPDYC 16

RESULT 7
 ID HSTR_ECOLI STANDARD; PRT: 18 AA.
 AC P01360;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Heat-stable enterotoxin ST-2 (ST-B).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=042;K86:H37 / 18D.
 RX MEDLINE=81264411; PubMed=7021541;
 RA Chan S.-K., Giannelis R.A.;
 RA "Amino acid sequence of heat-stable enterotoxin produced by
 RT Escherichia coli pathogenic for man.";
 RL J. Biol. Chem. 256:7744-7746(1981).
 RN [2]
 RP DISULFIDE BONDS.
 RX MEDLINE=87191003; PubMed=3552731;
 RA Shimonishi Y., Hidak Y., Koizumi M., Hane M., Almoto S., Takeda T.,
 RA Miwatani T., Takeda Y.;
 RT "Mode of disulfide bond formation of a heat-stable enterotoxin (StH)
 RT produced by a human strain of enterotoxigenic Escherichia coli.";
 RL FEBS Lett. 215:165-170(1987).
 CC -1- FUNCTION: TOXIN WHICH ACTIVATES THE PARTICULATE FORM OF GUANYLATE
 CC CYCLASE AND INCREASES CYCLIC GMP LEVELS WITHIN THE HOST
 CC INTESTINAL EPITHELIAL CELLS.
 CC -1- DISEASE: BOTH HEAT-STABLE AND HEAT-LABILE ENTEROTOXINS ARE
 CC PRODUCED BY PATHOGENIC STRAINS OF E. COLI AND AFFECT THE DIGESTIVE
 CC TRACT OF MAMMALS.
 CC -1- SIMILARITY: BELONGS TO THE HEAT-STABLE ENTEROTOXIN FAMILY.
 DR PIR: A01823; QHEC2.
 DR HSP: P01359; IETN.
 DR Interpro: IPR001489; Enterotoxin_HS.
 DR Pfam: PF02048; Enterotoxin_HS; 1.
 DR PROSITE: PS00273; ENTEROTOXIN_H_STABLE; 1.
 KM Toxin; Enterotoxin.
 FT DISULFID 5 10
 FT DISULFID 6 14
 FT DISULFID 9 17
 FT DISULFID 14 17
 SQ SEQUENCE 18 AA: 1978 MW: D0C975F49D600650 CRC64;
 Query Match 21.9%; Score 25; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCY 3
 DB 9 CCY 11

RESULT 8

LCRP_PETMA
ID LCRP_PETMA STANDARD: PRT: 19 AA.
AC 010936;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Corticostatin-related protein LCRP.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
NX NCBI_Taxid=7757;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=96321324; PubMed=8759287;
RA Conlon J.M., Sower S.A.;
RT "Isolation of a peptide structurally related to mammalian
corticosteroids from the lamprey *Petromyzon marinus*.";
RL Comp. Biochem. Physiol. 114B:133-137(1996).
CC -1- FUNCTION: MAY HAVE MICROBICIDAL ACTIVITIES. MAY INHIBIT
CORTICOTROPIN (ACTH) STIMULATED STEROIDOGENESIS AND THE MICROBIAL
ACTIONS OF THE CORTICOSTATINS.
CC -1- MASS SPECTROMETRY: MW=2201; MW_ERR=0.4; METHOD=Electrospray.
CC -1- SIMILARITY: BELONGS TO THE CORTICOSTATIN/DEFENSIN FAMILY.
KW Defensin; Antibiotic.
FT DISULFID 1 18 BY SIMILARITY.
FT DISULFID 3 9 BY SIMILARITY.
FT DISULFID 8 17 BY SIMILARITY.
SQ SEQUENCE 19 AA: 2209 MW: 8D9CEDC71A199A55 CRC64;

Query Match 21.9%; Score 25; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCYDQASY 8
| | | | |
Db 8 CCVAGLNV 15

RESULT 9
SCK3_LEIUO STANDARD: PRT: 14 AA.
ID SCK3_LEIUO
AC P45661;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Leinutotoxin III (Fragment).
OS Leinurus quinquenotatus quinquenotatus (Egyptian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butthidae; Butthidae; Leinurus.
NX NCBI_Taxid=6885;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93075256; PubMed=1280139;
RA Valdivia H.H., Martin B.M., Escobar L., Rossani L.D.;
RT "Noxiustoxin and leinutotoxin III, two homologous peptide toxins with
binding properties to synaptosomal membrane K⁺ channels.";
RL Biochem. Int. 27:953-962(1992).
CC -1- FUNCTION: BLOCKER OF POTASSIUM CHANNELS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
CHANNEL INHIBITORS SUBFAMILY.
DR InterPro: IPR001947; Scorpion_toxins.
DR PROSITE: PS01138; SCORP_SHORT_TOXIN; PARTIAL.
KW Neurotoxin; Potassium channel inhibitor.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA: 1588 MW: 83C67CCBD691205E CRC64;

Query Match 21.1%; Score 24; DB 1; Length 14;
Best Local Similarity 35.7%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

OY 2 CYDGASVNDTECE 15
| | | | |
Db 7 CYDSSQ-----CE 14

RESULT 10
SB60_MAIZE STANDARD: PRT: 20 AA.
ID SB60_MAIZE
AC P82868;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative 60 kDa spermidine-binding protein (fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
NX NCBI_Taxid=4577;
RN [1]
RP SEQUENCE, AND SUBCELLULAR LOCATION.
RC STRAIN=cv. Cecilia; TISSUE=Coleoptile;
RA Tassoni A., Napier R.M., Franceschetti M., Venis M.A., Bagni N.;
RT "Spermidine-binding proteins: purification and expression analysis in
Zea mays.";
RL Plant Physiol. 0:0-0(2002).
CC -1- SUBUNIT: Dimer of 18 kDa and 60 kDa subunit (Probable).
CC -1- SUBCELLULAR LOCATION: Mitochondrial membrane.
CC -1- MISCELLANEOUS: On the 2D-gel its MW is: 60 kDa.
KW Membrane; Microsome.
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA: 2093 MW: 7FD730C00391579A CRC64;

Query Match 21.1%; Score 24; DB 1; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.1e+02;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 6 ASVNDTECEQRAAR 20
| | | | |
Db 4 AVEPPEPTEQNRKAK 18

RESULT 11
CXAL_CONMA STANDARD: PRT: 14 AA.
ID CXAL_CONMA
AC P01521;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin MI (MI).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
NX NCBI_Taxid=6492;
RN [1]
RP SEQUENCE.
RX MEDLINE=83073458; PubMed=7149738;
RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
RT "Isolation and structure of a peptide toxin from the marine snail
Conus magus.";
RL Arch. Biochem. Biophys. 218:329-334(1982).
RN [2]
RP DISULFIDE BONDS.
RX MEDLINE=84032400; PubMed=6630187;
RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
RT "Conotoxin MI. Disulfide bonding and conformational states.";
RL J. Biol. Chem. 258:12247-12251(1983).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
INHIBIT THEM.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE

CC FAMILY.
DR PIR: A01784; NTRK1M.
DR HSSP: P56973; 1B45.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
FT Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 3 8
FT MOD.RES 4 14
SO SEQUENCE 14 AA; 1499 MW; DEEE91898BFE5BD CRC64;
AMIDATION.
Query Match 20.2%; Score 23; DB 1; Length 14;
Best Local Similarity 33.3%; Pred. No. 9.1e+02;
Matches 3; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCYDGSVN 9
DB 3 CCHPACGKN 11
RESULT 12
CXAL_CONIM STANDARD; PRT; 12 AA.
AC P50983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-conotoxin ImI.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conidae; Conidae; Conus.
OX NCBI_TaxID=35631;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RC TISSUE-VENOM.
RX MEDLINE=94266889; PubMed=8206995;
RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
Gray W.R., Oliveira B.M.;
RT "A nicotinic acetylcholine receptor ligand of unique specificity,
alpha-conotoxin ImI.";
RL J. Biol. Chem. 269:16733-16739(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95379776; PubMed=7651351;
RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
McIntosh J.M.;
RT "Alpha-conotoxin ImI exhibits subtype-specific nicotinic
acetylcholine receptor blockade: preferential inhibition of homomeric
alpha 7 and alpha 9 receptors.";
RL Mol. Pharmacol. 48:194-199(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99212205; PubMed=10194298;
RA Rogers J.P., Lugibuehl P., Shen G.S., McCabe R.T., Stevens R.C.,
Wemmer D.E.;
RT "NMR solution structure of alpha-conotoxin ImI and comparison to
other conotoxins specific for neuronal nicotinic acetylcholine
receptors.";
RL Biochemistry 38:3874-3882(1999).
RN [4]
RP STRUCTURE BY NMR.
RX PubMed=10350614;
RA Gouda H., Hirose S.;
RT "Solution structure of alpha-conotoxin ImI determined by
two-dimensional NMR spectroscopy.";
RL Biochim. Biophys. Acta 1431:384-394(1999).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=99158061; PubMed=10050774;
RA Maslennikov I.V., Shenkarev Z.O., Zhmak M.N., Ivanov V.T.,
Mettlesess C., Tseclin V.I., Arseniev A.S.;
RT "NMR spatial structure of alpha-conotoxin ImI reveals a common
scaffold in small and snake toxins recognizing neuronal nicotinic
acetylcholine receptors.";

RL FEBS Lett. 444:275-280(1999).
RN [6]
RP STRUCTURE BY NMR.
RX PubMed=10431825;
RA Lamthanh H., Jegou-Matheron C., Servent D., Menez A., Lancelin J.-M.,
RT "Minimal conformation of the alpha-conotoxin ImI for the alpha7
neuronal nicotinic acetylcholine receptor recognition: correlated CD,
NMR and binding studies.";
RL FEBS Lett. 454:293-298(1999).
RN [7]
RP STRUCTURE BY NMR.
RX MEDLINE=99324017; PubMed=10395477;
RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
RT "Solution structure of alpha-conotoxin ImI by 1H nuclear magnetic
resonance.";
RL J. Med. Chem. 42:2364-2372(1999).
RN [8]
RP MUTAGENESIS OF ASP-5; ARG-7 AND ARG-11, AND STRUCTURE BY NMR OF THESE
THREE MUTANTS.
RX PubMed=11124036;
RA Rogers J.P., Lugibuehl P., Pemberton K., Hartly P., Wemmer D.E.,
Stevens R.C.;
RT "Structure-activity relationships in a peptidic alpha7 nicotinic
acetylcholine receptor antagonist.";
RL J. Mol. Biol. 304:911-926(2000).
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
bind to the nicotinic acetylcholine receptors (nAChR) and thus
inhibit them. It is highly active against the neuromuscular
receptor in frog but not in mice. In contrast, it induces seizures
when injected centrally in mice and rats. It targets neuronal
nAChRs in mammals. It blocks homomeric alpha-7 nicotinic receptors
with 8-fold lower affinity. It has no effect on receptors composed
of alpha-2/beta-2, alpha-3/beta-2, alpha-4/beta-2, alpha-2/beta-4,
alpha-3/beta-4, or alpha-4/beta-4 subunit combinations.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
FAMILY.
DR PDB: 1IM1; 15-JUN-99.
DR PDB: 1IM1; 23-APR-99.
DR PDB: 1CNL; 27-MAY-99.
DR PDB: 1E74; 27-DEC-00.
DR PDB: 1E75; 27-DEC-00.
DR PDB: 1E76; 27-DEC-00.
DR PDB: 1G2G; 08-NOV-00.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.
FT DISULFID 2 8
FT MOD.RES 3 12
FT MUTAGEN 5 5
FT MUTAGEN 7 7
FT MUTAGEN 11 11
SQ SEQUENCE 12 AA; 1357 MW; 9C29CEA545A1176A CRC64;
Query Match 19.3%; Score 22; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCYD 4
DB 2 CCSD 5
RESULT 13
UN01_PINPS STANDARD; PRT; 15 AA.
ID UN01_PINPS
AC P81106;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (S1247/S1248) (N150/N151)

DE (Fragment).
 OS Pinus pinaster (Maritime pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 XX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC Tissue=Needle;
 RA Plomion C., Costa P., Bahman N., Frigerio J.M.;
 RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
 RT dominant and codominant protein markers assayed on diploid tissue, in
 RT a haploid-based genetic map";
 RL Silvae Genetica 46:161-165(1997).
 RN [2]
 RP SEQUENCE.
 RC Tissue=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins";
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.5, ITS MW IS: 62 kDa.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;
 Query Match 18.4%; Score 21; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 26+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 SYNDE 12
 Db 9 SATNDE 14

RESULT 14
 CXAB_CONAL STANDARD; PRT; 16 AA.
 AC P56641;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin Auitc.
 OS Conus aulticus (Court cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 XX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC Tissue=Venom;
 RA MEDLINE=99003392; PubMed=9786965;
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,
 RA Olivera B.M., McIntosh J.M.;
 RT "Alpha-conotoxin Auitc selectively blocks alpha3 beta4 nicotinic
 RT acetylcholine receptors and nicotine-evoked norepinephrine release";
 RL Neurosci. 18:8571-8579(1998).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. THIS PEPTIDE BLOCKS MAMMALIAN NICOTINIC
 CC ACETYLCHOLINE RECEPTORS COMPOSED OF ALPHA-3/BETA-4 SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1667.6; METHOD-Electrospray.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR HSP: P50984; IPE.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 3 16
 MOD_RES 4 16
 AMIDATION.

SQ SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;
 Query Match 18.4%; Score 21; DB 1; Length 16;
 Best Local Similarity 28.6%; Pred. No. 2.1e+03;
 Matches 4; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETC 14
 Db 3 CSYPCFATNSGYC 16

RESULT 15
 CXAB_CONPE STANDARD; PRT; 16 AA.
 AC P50985;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin PnIB.
 OS Conus pennaceus (Feathered cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 XX NCBI_TaxID=37335;
 RN [1]
 RP SEQUENCE.
 RC Tissue=Venom;
 RX MEDLINE=94347719; PubMed=8068627;
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
 RA Spira M.E., Zlotkin E.;
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
 RT acetylcholine receptors";
 RL Biochemistry 33:9523-9529(1994).
 RN [2]
 RP SULFATION OF TYR-15.
 RX MEDLINE=99242956; PubMed=10226369;
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
 RA Baldwin M.A., Burlingame A.L.;
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
 RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
 RT phosphopeptides by electrospray, matrix-assisted laser
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
 RT spectrometry";
 RL J. Mass Spectrom. 34:447-454(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
 RA MEDLINE=9744332; PubMed=9298951;
 RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
 RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
 RT comparison with alpha-conotoxins PnIA and GI";
 RL Biochemistry 36:11323-11330(1997).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM. IN CONTRAST TO OTHER ALPHA-CONOTOXINS, WHICH ARE
 CC SELECTIVE FOR VERTEBRATE SKELETAL MUSCLE NACHR, THE CONUS
 CC PENNACEUS ALPHA-CONOTOXINS BLOCK NACHR IN MOLLUSKS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PDB: 1AKG; 20-MAY-98.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
 FT DISULFID 2 8
 FT DISULFID 3 16
 FT MOD_RES 15 15
 FT MOD_RES 16 16
 MOD_RES 16 16
 AMIDATION.
 SQ SEQUENCE 16 AA; 1643 MW; 05310F95ED86AF5 CRC64;
 Query Match 18.4%; Score 21; DB 1; Length 16;
 Best Local Similarity 21.4%; Pred. No. 2.1e+03;
 Matches 5; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETC 14

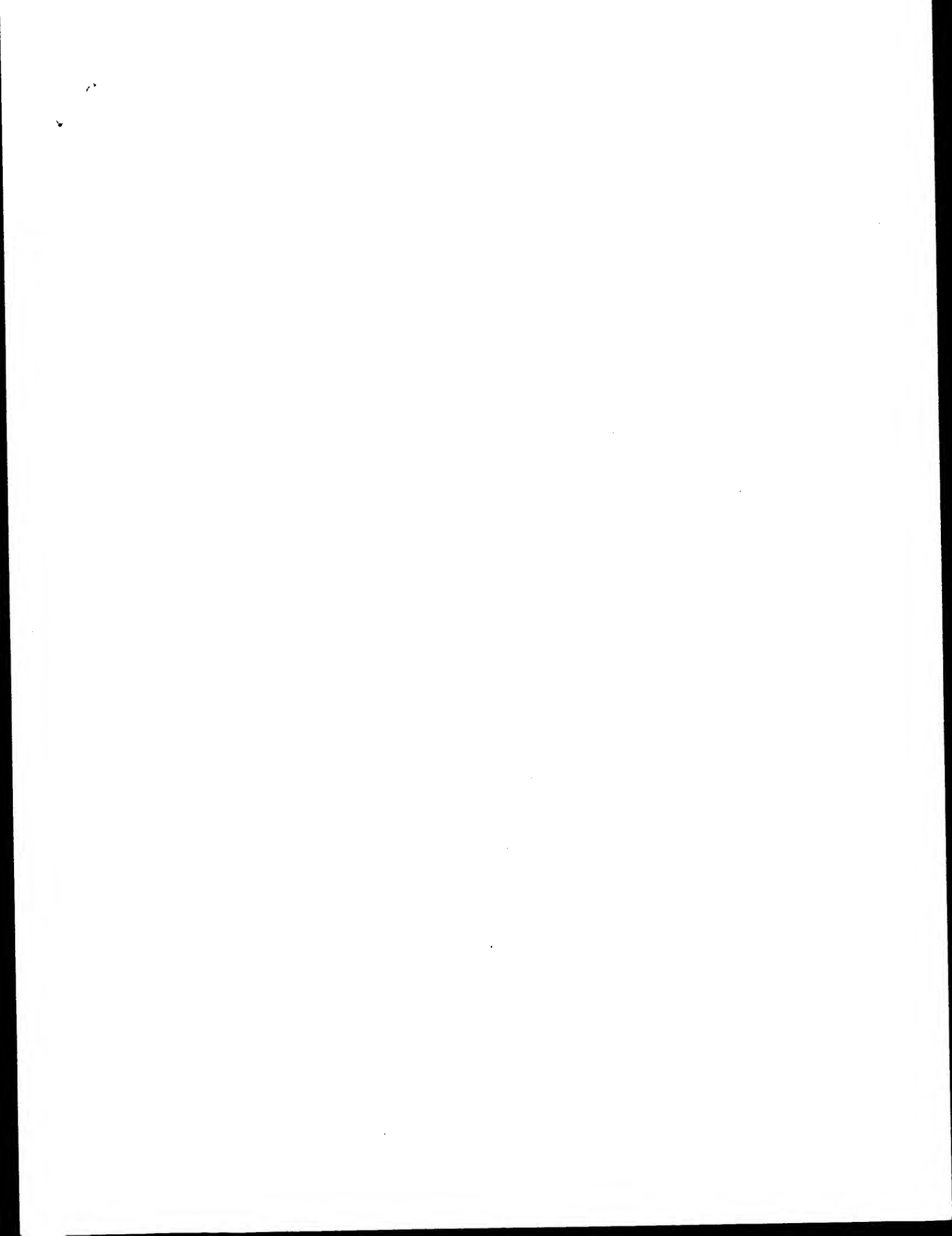
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Db 3 CSUPPCALSNPDYC 16

Search completed: May 1, 2003, 22:26:44
Job time : 27 secs



GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:23:02 ; Search time 28 Seconds
(without alignments)
147.177 Million cell updates/sec

Title: US-09-651-685A-5
Perfect score: 114
Sequence: 1 CCYDGSVNNDETCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 6395

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mnc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	24.6	19	11	Q9QVJ9
2	26	22.8	16	6	Q8SPT4
3	26	22.8	17	15	Q78381
4	26	22.8	18	6	O46665
5	26	22.8	19	4	Q9UCD0
6	26	22.8	19	4	Q9UCD0
7	25	21.9	15	4	Q9UCD0
8	24	21.1	18	6	Q9T781
9	24	21.1	20	5	P82201
10	24	21.1	18	2	O30888
11	23	20.2	18	2	O9R4F3
12	23	20.2	18	6	O9R4F3
13	23	20.2	19	2	O9R511
14	23	20.2	19	2	O9R511
15	23	20.2	19	2	O9R511
16	22.5	19.7	16	2	O47605

17	22	19.3	10	2	P96421	P96421 neisseria g
18	22	19.3	12	12	O85666	O85666 reovirus (t
19	22	19.3	15	11	O9QV87	O9QV87 rattus sp.
20	22	19.3	15	11	O9QV86	O9QV86 rattus sp.
21	22	19.3	18	4	O9UM83	O9UM83 homo sapien
22	22	19.3	18	6	O95MX1	O95MX1 syncerus ca
23	22	19.3	18	6	O95MX0	O95MX0 tragelaphus
24	22	19.3	18	6	O95MX9	O95MX9 oryx gazell
25	22	19.3	18	6	O95MX8	O95MX8 oryx dammah
26	22	19.3	18	6	O95MX7	O95MX7 hippotragus
27	22	19.3	18	6	O95MX6	O95MX6 bestragus h
28	22	19.3	18	6	O95MX5	O95MX5 alcelaphus
29	22	19.3	18	6	O95MX4	O95MX4 connochaete
30	22	19.3	18	6	O95MX3	O95MX3 redunda ful
31	22	19.3	18	6	O95MX2	O95MX2 redunda red
32	22	19.3	18	6	O95MX1	O95MX1 kobus leche
33	22	19.3	18	6	O95MX0	O95MX0 pelae capre
34	22	19.3	18	6	O95MX9	O95MX9 antidorcas
35	22	19.3	18	6	O95MX8	O95MX8 litocranius
36	22	19.3	18	6	O95MX7	O95MX7 raphicerus
37	22	19.3	18	6	O95MX6	O95MX6 raphicerus
38	22	19.3	18	6	O95MX5	O95MX5 raphicerus
39	22	19.3	18	6	O95MX4	O95MX4 neotragus m
40	22	19.3	18	6	O95MX3	O95MX3 oreotragus
41	22	19.3	18	6	O95MX2	O95MX2 cephalophus
42	22	19.3	18	6	O95MX1	O95MX1 sylvicapra
43	22	19.3	18	6	O95MX0	O95MX0 outrebia our
44	22	19.3	18	11	O63136	O63136 rattus norv
45	22	19.3	19	2	O35502	O35502 lactobacill

ALIGNMENTS

RESULT 1

ID	Q9QVJ9	PRELIMINARY:	PRT:	19 AA.
AC	Q9QVJ9	01-MAY-2000 (TREMBLREL. 13, Created)		
DT	01-MAY-2000 (TREMBLREL. 13, Last sequence update)			
DT	01-JUN-2002 (TREMBLREL. 21, Last annotation update)			
DE	Meprin-B peptide BI (Fragment).			
OS	Mus sp.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10095;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE-91373354; PubMed-1894622;			
RA	Koumas M.Z., Wolz R.L., Gorbea C.M., Bond J.S.;			
RT	"Meprin-A and -B, Cell surface endopeptidases of the mouse kidney.";			
RL	J. Biol. Chem. 266:17350-17357(1991).			
FT	NON_TER 1			
FT	NON_TER 19			
FT	NON_TER 19			
SO	SEQUENCE 19 AA; 2157 MW; 81666F19417E20C5 CRC64;			

Query Match

Best Local Similarity 24.6%; Score 28; DB 11; Length 19;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 3 YDGSVNNDET 13
Db 1 ENQVSIINDT 11

RESULT 2

ID Q8SPT4 PRELIMINARY: PRT: 16 AA.
AC Q8SPT4
DT 01-JUN-2002 (TREMBLREL. 21, Created)
DT 01-JUN-2002 (TREMBLREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLREL. 21, Last annotation update)
DE Chloride channel 2 (Fragment).

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GN CLC2.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Norrgren R.B. Jr., Zink M.A., Jia Y., Ojeda S.R., Spindel E.R.;
RT "Construction of a targeted Rhesus macaque microarray.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF489851; AAL96695.1; -.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1691 MW; 50D83BF4FC6AF49E CRC64;

Query Match 22.8%; Score 26; DB 6; Length 16;
Best Local Similarity 25.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 4 DGASVNDDECEOR 15
DB 5 EGSPSDSDCKQ 16

RESULT 3
078381 PRELIMINARY; PRT; 17 AA.
AC 078381;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Viral sample FLPBR5F (Florida patient B), partial env cds, V5 region
DE (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L.Q., Leigh-Brown A.J.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=92271245; PubMed=1589796;
RA Ou C.-Y., Ciesielski C.A., Myers G., Banda C.I., Luo C.C.,
RA Korber B.T.M., Mullins J.I., Schochetman G., Berkelman R.L.,
RA Economou A.N., Witte J.J., Furman L.J., Salten G.A., Curran J.W.,
RA Jaffe H.W.;
RT "Molecular Epidemiology of HIV Transmission in a Dental Practice.";
RL Science 256:1165-1171(1992).
DR EMBL; M92126; AAA44496.1; -.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1708 MW; 347570DD2D12CA370 CRC64;

Query Match 22.8%; Score 26; DB 15; Length 17;
Best Local Similarity 55.6%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 GASVNDDET 13
DB 2 GNNTNMTET 10

RESULT 4
046665 PRELIMINARY; PRT; 18 AA.
AC 046665;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (Fragment).
DR EMBL; G6PD.
RN [1]
RP Macroptus robustus robustus.

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=35580;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97224585; PubMed=9060417;
RA Loebel D.A., Johnston P.G.;
RT "Analysis of the intron-exon structure of the G6PD gene of the
RT wallaroo (Macropus robustus) by polymerase chain reaction.";
RL Mamm. Genome 8:146-147(1997).
DR EMBL; U53775; AAC48790.1; -.
DR InterPro; IPR001282; G6PD.
DR Pfam; PF02781; G6PD_C_1.
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 1992 MW; C6D5981B528258FB CRC64;

Query Match 22.8%; Score 26; DB 6; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.5e+03;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 6 ASVNDCEOR 17
DB 7 ASTNSDDVDRDK 18

RESULT 5
09UCD0 PRELIMINARY; PRT; 19 AA.
AC 09UCD0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE C215 antigen (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Bjork P., Jonsson U., Svedberg H., Larsson K., Lind P., Dillner J.,
RA Hedlund G., Donlsten M., Kalland T.;
RT "Isolation, partial characterization, and molecular cloning of a human
RT colon adenocarcinoma cell-surface glycoprotein recognized by the C215
RT mouse monoclonal antibody.";
RL J. Biol. Chem. 268:24232-24241(1993).
SQ SEQUENCE 19 AA; 2042 MW; 54135D12119705E6 CRC64;

Query Match 22.8%; Score 26; DB 4; Length 19;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DGASVND 11
DB 4 EGNLQND 11

RESULT 6
09QW83 PRELIMINARY; PRT; 19 AA.
AC 09QW83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE PHOSPHOPHORIN=PEPTIDE fragment 12-44 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=91291127; PubMed=2064607;

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RA Sabaay B., Stetler-Stevenson W.G., Lechner J.H., Veis A.;
RT "Domain structure and sequence distribution in dentin phosphoporyn.";
RL Biochem. J. 276:659-707(1991).
DR HSSP; P00760; 1A07.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2195 MW; 744603FE729FDE0C CRC64;

Query Match
Best Local Similarity 22.8%; Score 26; DB 11; Length 19;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 YDGASVND 11
Db 7 YNSNTLND 15

RESULT 7
09UCC0 PRELIMINARY; PRT; 15 AA.
AC 09UCC0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE Insulin-like growth factor receptor alpha subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=94079885; PubMed=8257668;
RA Kasuya J., Paz I.B., Maddux B.A., Goldfine I.D., Hefta S.A.,
RA Fujita-Yamaguchi Y.;
RT "Characterization of human placental insulin-like growth factor-
RT I/insulin hybrid receptors by protein microsequencing and
RT purification."
RL Biochemistry 32:13531-13536(1993).
SQ SEQUENCE 15 AA; 1721 MW; 98BC151D6D81784B CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 4; Length 15;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 CYDGASVND 11
Db 3 CGPGDIRND 12

RESULT 8
09TT81 PRELIMINARY; PRT; 18 AA.
AC 09TT81;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Wilm's tumor protein 1 (Fragment).
GN WT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21015404; PubMed=11330975;
RA Brouillette J.A., Andrew J.R., Venia P.J.;
RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
RT method."
RL Mamm. Genome 11:1079-1086(2000).
DR EMBL; AF201736; AAF19824.1; -.
FT NON_TER 1
FT NON_TER 18

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SQ SEQUENCE 18 AA; 2196 MW; 1EE8DAD8E072C0BF CRC64;

Query Match
Best Local Similarity 21.1%; Score 24; DB 6; Length 18;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 12 ETCEGRAR 20
Db 7 KTCQKRF 15

RESULT 9
Q16188 PRELIMINARY; PRT; 20 AA.
AC Q16188;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Adenosine deaminase protein (Fragment).
GN ADENOSINE DEAMINASE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94327968; PubMed=8051429;
RA Shovlin C.L., Simmonds H.A., Fairbanks L.D., Deacock S.J.,
RA Hughes J.M., Lechner R.I., Webster A.D., Sun X.M., Webb J.C.,
RA Soutar A.K.;
RT "Adult onset immunodeficiency caused by inherited adenosine deaminase
RT deficiency."
RL J. Immunol. 153:2331-2339(1994).
DR EMBL; S72469; AAD14102.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2175 MW; 4EAB6143F739B4C CRC64;

Query Match
Best Local Similarity 21.1%; Score 24; DB 4; Length 20;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 13 TCCEGRAR 20
Db 12 SCEVRCR 19

RESULT 10
P82201 PRELIMINARY; PRT; 20 AA.
AC P82201;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DE 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Bombycoidea; Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE.
RA STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
RT silkworm."
RL I Chuan Hsueh Pao 28:217-224(2001).
CC -1- SIMILARITY: TO THE N-TERMINAL OF TROPOMYOSINS.
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2215 MW; A3C1EPD3F1350767 CRC64;

Query Match
Best Local Similarity 21.1%; Score 24; DB 5; Length 20;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 CEORA 18
|||:|
Db 5 CEORA 9

RESULT 11

ID 030888 PRELIMINARY; PRT; 18 AA.
AC 030888;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Nodulation protein (Fragment).
GN NODA.
OS Bradyrhizobium sp.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=376;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20020861; PubMed=10553291;
RA Steiner J.P., Parker M.A.;
RT "Diversity and relationships of Bradyrhizobia from Amphicarpa
RT bracteaata based on partial nod and ribosomal sequences."
RL Syst. Appl. Microbiol. 22:387-392(1999).
DR EMBL; AF020680; AAB71696.1;
FT NON_TER 18
SQ SEQUENCE 18 AA; 1943 MW; C8C595DCD14D7A5F CRC64;

Query Match 20.2%; Score 23; DB 2; Length 18;
Best Local Similarity 28.6%; Pred. No. 4.8e+03;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 7 SYNNDETCEORAR 20
:::|:|:|
Db 2 NIPGSRSAESRSAR 15

RESULT 12

ID 094F3 PRELIMINARY; PRT; 18 AA.
AC 094F3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE 20 kDa fibrial adhesin subunit (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE.
RX MEDLINE=96110952; PubMed=8557360;
RA Berlin Y., Girardeau J.P., Darfeuille-Michaud A., Contrepoint M.;
RT "Characterization of 20k fimbria, a new adhesin of septicemic and
RT diarrhoea-associated Escherichia coli strains, that belongs to a family
RT of adhesins with N-acetyl-D-glucosamine recognition."
RL Infect. Immun. 64:332-342(1996).
SQ SEQUENCE 18 AA; 1990 MW; 79AF96A13476DF81 CRC64;

Query Match 20.2%; Score 23; DB 2; Length 18;
Best Local Similarity 35.7%; Pred. No. 4.8e+03;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 YDASVNNDETCEQ 16
|||:|:|
Db 1 YDGTINNGKVVQD 14

RESULT 13

097668

ID 097668 PRELIMINARY; PRT; 18 AA.

AC 097668;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Lactoferrin (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Brandon R.B., Giffard J.M., Bell T.R.;
RT "Isolation of Equine Lactoferrin Gene."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF102025; AAC77463.1;
DR HSSP; 077698; ICE2.
DR InterPro; IPR001156; Transferrin.
DR Pfam; PF00405; transferrin; 1.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1936 MW; D8FBFA226AA6DD9 CRC64;

Query Match 20.2%; Score 23; DB 6; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGA 6
|||
Db 1 CLQDGA 6

RESULT 14

ID 09R511 PRELIMINARY; PRT; 19 AA.
AC 09R511;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Nitrite hydratase alpha subunit (Fragment).
OS Brevibacterium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Micrococciaceae; Brevibacteriaceae.
OX NCBI_TaxID=1696;
RN [1]
RP SEQUENCE.
RX MEDLINE=92407758; PubMed=1527703;
RA Duran R., Chion C.K., Bigey F., Arnaud A., Galzy P.;
RT "The N-terminal amino acid sequences of Brevibacterium sp. R312
RT nitrite hydratase."
RL J. Basic Microbiol. 32:13-19(1992).
SQ SEQUENCE 19 AA; 1923 MW; 84726D1A1282FB63 CRC64;

Query Match 20.2%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 5.1e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 SYNNDETCEORA 18
|||:|:|
Db 1 SVTIDHTTENNA 12

RESULT 15

ID 09UDF5 PRELIMINARY; PRT; 20 AA.
AC 09UDF5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE DIPEPTIDYLPEPTIDASE IV (EC 3.4.14.5) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE
RX MEDLINE-95294018; PubMed-7539799;
RA Duke-Cohan J.S., Morimoto C., Rocker J.A., Schlossman S.F.;
RT "A novel form of dipeptidylpeptidase IV found in human serum.
RT Isolation, characterization, and comparison with T lymphocyte membrane
RT dipeptidylpeptidase IV (CD26).";
RL J. Biol. Chem. 270:14107-14114(1995).
SQ SEQUENCE 20 AA; 2274 MW; 764B669537DB8AB0 CRC64;

Query Match 20.2%; Score 23; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 5.4e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 CYDGASVND 11
|| : ||
Db 7 CYCTANTND 16

Search completed: May 1, 2003, 22:27:18
Job time : 29 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:20:12 ; Search time 74 Seconds

(without alignments)
36.014 Million cell updates/sec

Title: US-09-651-685a-5
Perfect score: 114
Sequence: 1 CCGDASVNDTECEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 289567

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	22	AA874055 Human C5a peptide
2	111	97.4	20	22	AA874111 C-terminal truncat
3	110	96.5	20	22	AA874110 C-terminal truncat
4	110	96.5	20	22	AA874112 C-terminal truncat
5	110	96.5	20	22	AA874113 C-terminal truncat
6	110	96.5	20	22	AA874114 C-terminal truncat
7	110	96.5	20	22	AA874115 C-terminal truncat
8	109	95.6	19	22	AA874097 C-terminal truncat
9	109	95.6	20	22	AA874120 Human C3a peptide
10	108	94.7	20	22	AA874107 C-terminal truncat

11	108	94.7	20	22	AA874108 C-terminal truncat
12	106	93.0	20	22	AA874115 C-terminal truncat
13	105	92.1	18	22	AA874098 C-terminal truncat
14	105	92.1	19	22	AA874102 C-terminal truncat
15	102	89.5	20	22	AA874109 C-terminal truncat
16	101	88.6	17	22	AA874099 C-terminal truncat
17	98	86.0	20	22	AA874117 C-terminal truncat
18	96	84.2	16	22	AA874100 C-terminal truncat
19	96	84.2	18	22	AA874103 C-terminal truncat
20	91	79.8	15	22	AA874104 C-terminal truncat
21	89	78.1	17	22	AA874105 C-terminal truncat
22	83	72.8	15	22	AA874106 C-terminal truncat
23	77	67.5	15	22	AA874052 C-terminal truncat
24	51	44.7	20	22	AA874052 C-terminal truncat
25	40.5	35.5	18	21	AA821536 Cone snail alpha-c
26	38.5	33.8	16	21	AA821533 Cone snail alpha-c
27	38.5	33.8	20	21	AA821498 Cone snail alpha-c
28	38	33.3	16	16	AA821522 Cone snail alpha-c
29	38	33.3	16	21	AA808449 Cone snail alpha-c
30	36	31.6	15	23	AA821549 Cone snail alpha-c
31	35.5	31.1	17	21	AA821549 Cone snail alpha-c
32	35	30.7	16	18	AA821549 Cone snail alpha-c
33	35	30.7	16	18	AA821549 Cone snail alpha-c
34	34.5	30.3	18	16	AA821736 Cone snail alpha-c
35	34.5	30.3	18	18	AA821736 Cone snail alpha-c
36	34.5	30.3	18	18	AA821736 Cone snail alpha-c
37	34	29.8	15	18	AA821751 Cone snail alpha-c
38	34	29.8	15	18	AA821751 Cone snail alpha-c
39	34	29.8	19	15	AA856639 Tyrosine activatio
40	34	29.8	19	15	AA856633 Tyrosine activatio
41	34	29.8	19	16	AA856633 Tyrosine activatio
42	34	29.8	19	18	AA830153 Tandem SH2 ligand
43	34	29.8	19	18	AA830153 Tandem SH2 ligand
44	34	29.8	19	18	AA821743 Tandem SH2 ligand
45	33.5	29.4	18	21	AA821411 Cone snail alpha-c
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ALIGNMENTS

RESULT 1
ID AAB74055 standard; Peptide; 20 AA.
AC AAB74055;
DT 16-MAY-2001 (first entry)
XX
DE Human C5a peptide fragment #2.
XX
KW Human; C5a; complement; antibody; bacterial infection; sinusitis;
KW meningitis; respiratory; gastrointestinal; urinary tract infection;
KW wound; anaphylatoxin; sepsis.
XX
OS Homo sapiens.
XX
PN WO200115731-A1.
XX
PD 08-MAR-2001.
XX
PF 31-AUG-2000; 2000MO-US24219.
XX
PR 31-AUG-1999; 99US-0387671.
XX
(UNMI) UNIV MICHIGAN.
XX
PI Ward PA, Huber-Lang M, Sarma V;
XX WPI: 2001-226665/23.
XX N-PSDB: AAF75793.
XX
PT Compositions for treating blood-borne and toxin mediated diseases and treatment of sepsis in humans and other animals comprises anti-C5a

PT antibodies generated against C-terminal truncated C5a peptides -
XX
PS Claim 8; Page 26; 84pp; English.

CC The present sequence is a peptide fragment of human complement component
CC C5a (the full-length sequence is given in AAB74053). The present
CC invention relates to an antibody specific for the present sequence. The
CC C5a-antibody can be used in a therapeutic composition, which is useful
CC for treating a subject suffering from bacterial infection, e.g.
CC sinusitis, meningitis, respiratory, gastrointestinal or urinary tract
CC infections or infections in wounds. In addition, the C5a antibody can
CC be used for treating sepsis. C5a is also known as anaphylatoxin.
XX

XX Sequence 20 AA;

Query Match 100.0%; Score 114; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTECEQRAAR 20
DB 1 CCYDGASVNDTECEQRAAR 20

RESULT 2

AAB74111
ID AAB74111 standard; Peptide; 20 AA.

XX AAB74111;

XX 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #49.

XX C5a; complement; antibody; bacterial infection; sinusitis;
XX meningitis; respiratory; gastrointestinal; urinary tract infection;
XX wound; anaphylatoxin; sepsis.

XX Unidentified.

XX WO200115731-A1.

XX 08-MAR-2001.

PF 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI; 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
XX treatment of sepsis in humans and other animals comprises anti-C5a
XX antibodies generated against C-terminal truncated C5a peptides -

XX Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
XX present invention relates to an antibody specific for the present
XX sequence. The C5a-antibody can be used in a therapeutic composition,
XX which is useful for treating a subject suffering from bacterial
XX infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
XX urinary tract infections or infections in wounds. In addition, the C5a
XX antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.

XX Sequence 20 AA;

Query Match 97.4%; Score 111; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.3e-10;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTECEQRAAR 20
DB 1 CCYDGASVNDTECEQRAAR 20

RESULT 3

AAB74110
ID AAB74110 standard; Peptide; 20 AA.

XX AAB74110;

XX 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #48.

XX C5a; complement; antibody; bacterial infection; sinusitis;
XX meningitis; respiratory; gastrointestinal; urinary tract infection;
XX wound; anaphylatoxin; sepsis.

XX Unidentified.

XX WO200115731-A1.

XX 08-MAR-2001.

PF 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI; 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
XX treatment of sepsis in humans and other animals comprises anti-C5a
XX antibodies generated against C-terminal truncated C5a peptides -

XX Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
XX present invention relates to an antibody specific for the present
XX sequence. The C5a-antibody can be used in a therapeutic composition,
XX which is useful for treating a subject suffering from bacterial
XX infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
XX urinary tract infections or infections in wounds. In addition, the C5a
XX antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.

XX Sequence 20 AA;

Query Match 96.5%; Score 110; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNDTECEQRAAR 20
DB 1 CCYDGASVNDTECEQRAAR 20

RESULT 4

AAB74112
ID AAB74112 standard; Peptide; 20 AA.

XX AAB74112;

XX 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #50.

XX	WPI; 2001-226665/23.
DR	
XX	Compositions for treating blood-borne and toxin mediated diseases and
PT	treatment of sepsis in humans and other animals comprises anti-C5a
PT	antibodies generated against C-terminal truncated C5a peptides -
XX	
PS	Disclosure; Page 30; 84pp; English.
XX	
CC	The present sequence is a C-terminal truncated C5a peptide fragment. The
CC	present invention relates to an antibody specific for the present
CC	sequence. The C5a-antibody can be used in a therapeutic composition,
CC	which is useful for treating a subject suffering from bacterial
CC	infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC	urinary tract infections or infections in wounds. In addition, the C5a
CC	antibody can be used for treating sepsis. C5a is also known as
XX	anaphylatoxin.
XX	
SQ	Sequence 20 AA:
QY	Query Match 96.5%; Score 110; DB 22; Length 20;
	Best Local Similarity 95.0%; Pred. No. 1.9e-10;
	Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	1 CCYDGSANNDTCRCRAR 20
	1 CCYDGSANNDTCRCRAR 20
XX	
RESULT 6	
AA874114	
ID	AA874114 standard; Peptide; 20 AA.
XX	
AC	AA874114;
XX	
DT	16-MAY-2001 (first entry)
XX	
DE	C-terminal truncated C5a peptide #52.
XX	
C5a; complement; antibody; bacterial infection; sinusitis;	
meningitis; respiratory; gastrointestinal; urinary tract infection;	
wound; anaphylatoxin; sepsis.	
XX	
XX	Unidentified.
OS	
XX	
PN	WO200115731-A1.
XX	
PD	08-MAR-2001.
XX	
PF	31-AUG-2000; 2000WO-US24219.
XX	
PR	31-AUG-1999; 99US-0387671.
XX	
AA	(UNMI) UNIV MICHIGAN.
XX	
PL	Ward PA, Huber-Iang M, Sarma V;
XX	
DR	WPI: 2001-226665/23.
XX	
CC	Compositions for treating blood-borne and toxin mediated diseases and
CC	treatment of sepsis in humans and other animals comprises anti-C5a
PT	antibodies generated against C-terminal truncated C5a peptides -
XX	
PS	Disclosure; Page 30; 84pp; English.
XX	
CC	The present sequence is a C-terminal truncated C5a peptide fragment. The
CC	present invention relates to an antibody specific for the present
CC	sequence. The C5a-antibody can be used in a therapeutic composition,
CC	which is useful for treating a subject suffering from bacterial
CC	infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC	urinary tract infections or infections in wounds. In addition, the C5a
CC	antibody can be used for treating sepsis. C5a is also known as
CC	anaphylatoxin.

XX
SQ Sequence 20 AA;

Query Match 96.5%; Score 110; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETCEQRAR 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCYDGASVNNDETCEQRAR 20

RESULT 7
AAB74116

ID AAB74116 standard; Peptide: 20 AA.

AC AAB74116;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #54.

XX C5a; complement; antibody; bacterial infection; sinusitis;

KW meningitis; respiratory; gastrointestinal; urinary tract infection;

KW wound; anaphylatoxin; sepsis.

XX Unidentified.

XX WO200115731-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI; 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
PT treatment of sepsis in humans and other animals comprises anti-C5a
PT antibodies generated against C-terminal truncated C5a peptides -

XX Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
CC present invention relates to an antibody specific for the present
CC sequence. The C5a-antibody can be used in a therapeutic composition,
CC which is useful for treating a subject suffering from bacterial
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC urinary tract infections or infections in wounds. In addition, the C5a
CC antibody can be used for treating sepsis. C5a is also known as
CC anaphylatoxin.

XX Sequence 20 AA;

Query Match 96.5%; Score 110; DB 22; Length 20;
Best Local Similarity 95.0%; Pred. No. 1.9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETCEQRAR 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCYDGASVNNDETCEQRAR 20

RESULT 8
AAB74097

ID AAB74097 standard; Peptide: 19 AA.

XX AAB74097;

XX 16-MAY-2001 (first entry)

XX C-terminal truncated C5a peptide #35.

XX C5a; complement; antibody; bacterial infection; sinusitis;

KW meningitis; respiratory; gastrointestinal; urinary tract infection;

KW wound; anaphylatoxin; sepsis.

XX Unidentified.

XX WO200115731-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNIV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI; 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
PT treatment of sepsis in humans and other animals comprises anti-C5a
PT antibodies generated against C-terminal truncated C5a peptides -
XX Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
CC present invention relates to an antibody specific for the present
CC sequence. The C5a-antibody can be used in a therapeutic composition,
CC which is useful for treating a subject suffering from bacterial
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC urinary tract infections or infections in wounds. In addition, the C5a
CC antibody can be used for treating sepsis. C5a is also known as
CC anaphylatoxin.

XX Sequence 19 AA;

Query Match 95.6%; Score 109; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETCEQRA 19
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCYDGASVNNDETCEQRA 19

RESULT 9
AAB74120

ID AAB74120 standard; Peptide: 20 AA.

XX AAB74120;

XX 16-MAY-2001 (first entry)

XX Human C5a peptide fragment #7.

KW Human; C5a; complement; antibody; bacterial infection; sinusitis;

KW meningitis; respiratory; gastrointestinal; urinary tract infection;

KW wound; anaphylatoxin; sepsis.

XX Homo sapiens.

XX WO200115731-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000WO-US24219.

RESULT 12
AAB74115 standard; Peptide: 20 AA.
AC AAB74115;
DT 16-MAY-2001 (first entry)
DE C-terminal truncated C5a peptide #53.
KW C5a; complement; antibody; bacterial infection; sinusitis;
KM meningitis; respiratory; gastrointestinal; urinary tract infection;
XX wound; anaphylatoxin; sepsis.
OS Unidentified.
XX WO200115731-A1.
XX PD 08-MAR-2001.
XX PF 31-AUG-2000; 2000WO-US24219.
XX PR 31-AUG-1999; 99US-0387671.
XX PA (UNMI) UNIV MICHIGAN.
XX PI Ward PA, Huber-Lang M, Sarma V;
XX DR WPI; 2001-226665/23.
XX DT
XX PT Compositions for treating blood-borne and toxin mediated diseases and
XX treatment of sepsis in humans and other animals comprises anti-C5a
XX antibodies generated against C-terminal truncated C5a peptides -
PS Disclosure; Page 30; 84pp; English.
XX
XX The present sequence is a C-terminal truncated C5a peptide fragment. The
XX present invention relates to an antibody specific for the present
XX sequence. The C5a-antibody can be used in a therapeutic composition,
XX which is useful for treating a subject suffering from bacterial
XX infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
XX urinary tract infections or infections in wounds. In addition, the C5a
XX antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.
SQ Sequence 20 AA;
Query Match 93.0%; Score 106; DB 22; Length 20;
Best Local Similarity 90.0%; Pred. No. 8, 1e-10;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCYDGASVNNDETCQRAAR 20
DB 1 CCYDGASVNNDETCQRYVR 20
RESULT 13
AAB74098
ID AAB74098 standard; Peptide: 18 AA.
AC AAB74098;
DT 16-MAY-2001 (first entry)
DE C-terminal truncated C5a peptide #36.
KW C5a; complement; antibody; bacterial infection; sinusitis;
KM meningitis; respiratory; gastrointestinal; urinary tract infection;
XX wound; anaphylatoxin; sepsis.
OS Unidentified.
XX WO200115731-A1;
XX PN

XX
XX PD 08-MAR-2001.
XX PF 31-AUG-2000; 2000WO-US24219.
XX PR 31-AUG-1999; 99US-0387671.
XX PA (UNMI) UNIV MICHIGAN.
XX PI Ward PA, Huber-Lang M, Sarma V;
XX DR WPI; 2001-226665/23.
XX DT
XX PT Compositions for treating blood-borne and toxin mediated diseases and
XX treatment of sepsis in humans and other animals comprises anti-C5a
XX antibodies generated against C-terminal truncated C5a peptides -
PS Disclosure; Page 30; 84pp; English.
XX
XX The present sequence is a C-terminal truncated C5a peptide fragment. The
XX present invention relates to an antibody specific for the present
XX sequence. The C5a-antibody can be used in a therapeutic composition,
XX which is useful for treating a subject suffering from bacterial
XX infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
XX urinary tract infections or infections in wounds. In addition, the C5a
XX antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.
SQ Sequence 18 AA;
Query Match 92.1%; Score 105; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCYDGASVNNDETCQRA 18
DB 1 CCYDGASVNNDETCQRA 18
RESULT 14
AAB74102
ID AAB74102 standard; Peptide: 19 AA.
AC AAB74102;
DT 16-MAY-2001 (first entry)
DE C-terminal truncated C5a peptide #40.
KW C5a; complement; antibody; bacterial infection; sinusitis;
KM meningitis; respiratory; gastrointestinal; urinary tract infection;
XX wound; anaphylatoxin; sepsis.
OS Unidentified.
XX WO200115731-A1.
XX PN 08-MAR-2001.
XX PF 31-AUG-2000; 2000WO-US24219.
XX PR 31-AUG-1999; 99US-0387671.
XX PA (UNMI) UNIV MICHIGAN.
XX PI Ward PA, Huber-Lang M, Sarma V;
XX DR WPI; 2001-226665/23.
XX DT
XX PT Compositions for treating blood-borne and toxin mediated diseases and
XX treatment of sepsis in humans and other animals comprises anti-C5a
XX antibodies generated against C-terminal truncated C5a peptides -

PS Disclosure; Page 30; 84pp; English.

XX
CC The present sequence is a C-terminal truncated C5a peptide fragment. The
CC present invention relates to an antibody specific for the present
CC sequence. The C5a-antibody can be used in a therapeutic composition,
CC which is useful for treating a subject suffering from bacterial
CC infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
CC urinary tract infections or infections in wounds. In addition, the C5a
CC antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.

XX Sequence 19 AA:

Query Match 92.1%; Score 105; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 1,1e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CYDGASVNNDETCEQRAAR 20
DB 1 CYDGASVNNDETCEQRAAR 19

RESULT 15

AAB74109
ID AAB74109 standard; Peptide: 20 AA.

AC AAB74109;

DT 16-MAY-2001 (first entry)

DE C-terminal truncated C5a peptide #47.

XX C5a: complement; antibody; bacterial infection; sinusitis;
XX meningitis; respiratory; gastrointestinal; urinary tract infection;
XX wound; anaphylatoxin; sepsis.

OS Unidentified.

XX WO200115731-A1.

XX 08-MAR-2001.

XX 31-AUG-2000; 2000MO-US24219.

XX 31-AUG-1999; 99US-0387671.

XX (UNMI) UNTV MICHIGAN.

XX Ward PA, Huber-Lang M, Sarma V;

XX WPI: 2001-226665/23.

XX Compositions for treating blood-borne and toxin mediated diseases and
XX treatment of sepsis in humans and other animals comprises anti-C5a
XX antibodies generated against C-terminal truncated C5a peptides -

XX Disclosure; Page 30; 84pp; English.

XX The present sequence is a C-terminal truncated C5a peptide fragment. The
XX present invention relates to an antibody specific for the present
XX sequence. The C5a-antibody can be used in a therapeutic composition,
XX which is useful for treating a subject suffering from bacterial
XX infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or
XX urinary tract infections or infections in wounds. In addition, the C5a
XX antibody can be used for treating sepsis. C5a is also known as
XX anaphylatoxin.

XX Sequence 20 AA:

Query Match 89.5%; Score 102; DB 22; Length 20;

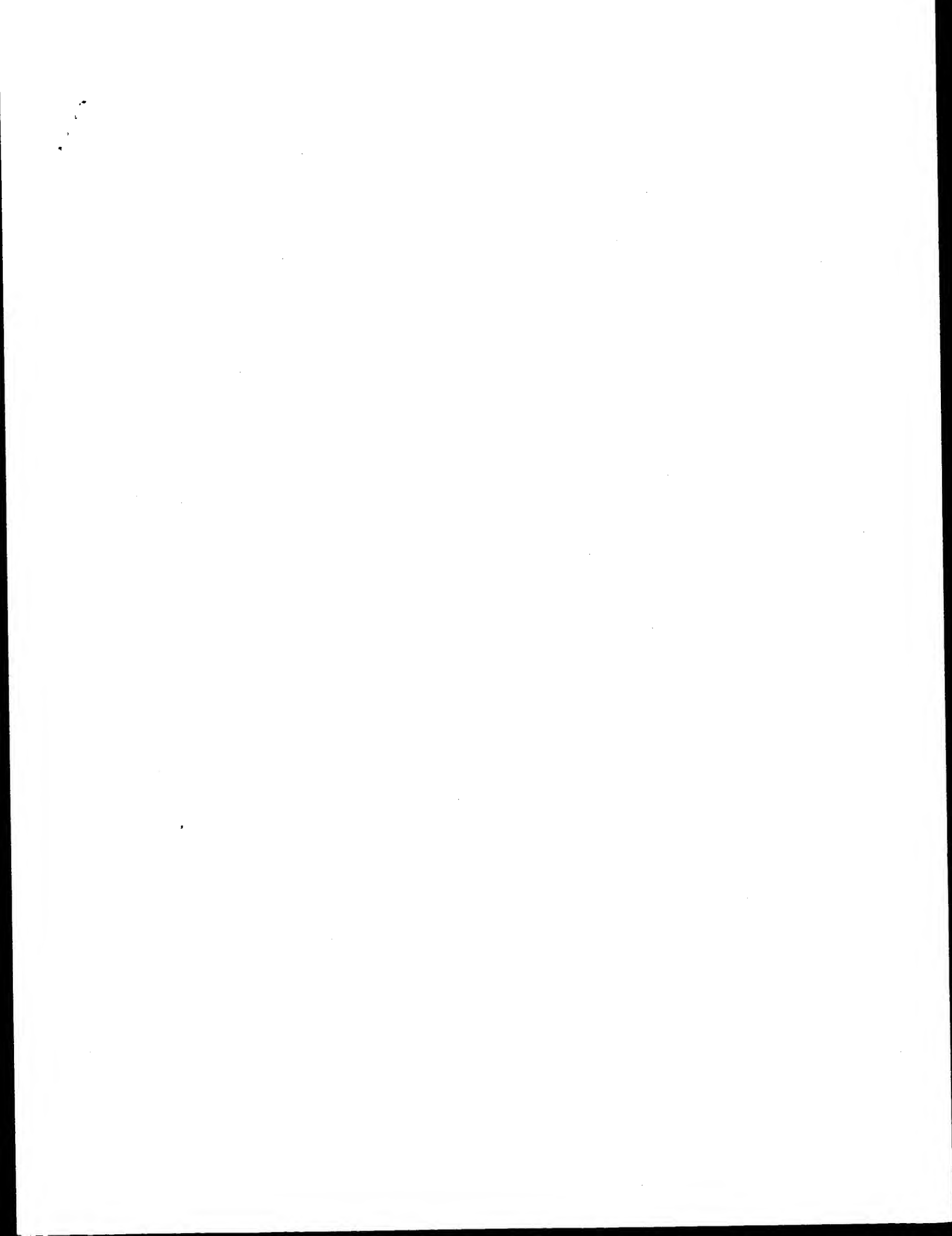
Best Local Similarity 90.0%; Pred. No. 3.4e-09;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETCEQRAAR 20

DB 1 CCYDGASVNNDETCEQRAAR 20

Search completed: May 1, 2003, 22:26:11
Job time : 75 secs



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:27:23 ; Search time 45 Seconds
(without alignments)
38.350 Million cell updates/sec

Title: US-09-651-685A-5
Sequence: 114
1 CCYDASVNNDETCEQRAAR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328255 segs, 86286685 residues
Total number of hits satisfying chosen parameters: 62178

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgnt2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgnt2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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14: /cgnt2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	9	US-09-878-603-5
2	111	97.4	20	9	US-09-878-603-68
3	110	96.5	20	9	US-09-878-603-67
4	110	96.5	20	9	US-09-878-603-69
5	110	96.5	20	9	US-09-878-603-70
6	110	96.5	20	9	US-09-878-603-71
7	110	96.5	20	9	US-09-878-603-72
8	109	96.5	20	9	US-09-878-603-73
9	108	94.7	20	9	US-09-878-603-54
10	108	94.7	20	9	US-09-878-603-65
11	106	93.0	20	9	US-09-878-603-72
12	105	92.1	18	9	US-09-878-603-55
13	105	92.1	19	9	US-09-878-603-59
14	102	89.5	20	9	US-09-878-603-56
15	101	88.6	17	9	US-09-878-603-56
16	98	86.0	20	9	US-09-878-603-74
17	96	84.2	16	9	US-09-878-603-57
18	96	84.2	18	9	US-09-878-603-60
19	91	79.8	15	9	US-09-878-603-58

20	89	78.1	17	9	US-09-878-603-61	Sequence 61, Appl
21	83	72.8	16	9	US-09-878-603-62	Sequence 62, Appl
22	77	67.5	15	9	US-09-878-603-63	Sequence 63, Appl
23	51	44.7	20	9	US-09-878-603-2	Sequence 2, Appl
24	34	29.8	20	10	US-09-321-801-5	Sequence 5, Appl
25	32	28.1	6	9	US-09-878-603-15	Sequence 15, Appl
26	30.5	26.8	16	9	US-10-084-994-16	Sequence 16, Appl
27	29	25.4	9	9	US-09-252-150-78	Sequence 78, Appl
28	29	25.4	10	10	US-09-908-741-108	Sequence 108, Appl
29	29	25.4	14	9	US-09-878-603-25	Sequence 25, Appl
30	28	24.6	6	9	US-09-878-603-27	Sequence 27, Appl
31	28	24.6	6	9	US-09-873-676-84	Sequence 84, Appl
32	28	24.6	11	10	US-09-873-676-32	Sequence 32, Appl
33	28	24.6	18	10	US-09-734-520-23	Sequence 23, Appl
34	28	24.6	18	12	US-10-012-034A-23	Sequence 23, Appl
35	28	24.6	20	10	US-09-731-221-66	Sequence 66, Appl
36	28	24.6	20	9	US-09-910-009A-211	Sequence 211, Appl
37	27.5	24.1	20	9	US-09-864-761-47743	Sequence 47743, A
38	27	23.7	17	10	US-09-854-188-8	Sequence 8, Appl
39	26.5	23.2	14	10	US-09-910-009A-370	Sequence 370, Appl
40	26.5	23.2	16	9	US-09-908-741-22	Sequence 22, Appl
41	26.5	23.2	18	9	US-09-878-603-24	Sequence 24, Appl
42	26	22.8	6	9	US-09-917-788-4	Sequence 4, Appl
43	26	22.8	7	9	US-09-917-788-4	Sequence 4, Appl
44	26	22.8	11	10	US-09-791-946-5	Sequence 5, Appl
45	26	22.8	12	9	US-10-156-932-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-878-603-5
; Sequence 5, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarna, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878, 603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387, 671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-878-603-5

Query Match 100.0% Score 114; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDASVNNDETCEQRAAR 20
DB 1 CCYDASVNNDETCEQRAAR 20

RESULT 2
US-09-878-603-68
; Sequence 68, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarna, Vidya
; APPLICANT: Czernak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis

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; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 68
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-68
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Query Match          97.4%; Score 111; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 6.4e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CCYDGASVNNDETCEQRAAR 20
        |||||:|||||
Db      1 CCYDGATVNNDETCEQRAAR 20
```

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RESULT 3
US-09-878-603-67
; Sequence 67, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czeremak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 67
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-67
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Query Match          96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 CCYDGASVNNDETCEQRAAR 20
        |||||:|||||
Db      1 CCYDGASVNNDETCEQRAAR 20
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RESULT 4
US-09-878-603-69
; Sequence 69, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czeremak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
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; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-69
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Query Match          96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 CCYDGASVNNDETCEQRAAR 20
        |||||:|||||
Db      1 CCYDGVSNNDETCEQRAAR 20
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RESULT 5
US-09-878-603-70
; Sequence 70, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czeremak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 70
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-70
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Query Match          96.5%; Score 110; DB 9; Length 20;
Best Local Similarity 95.0%; Pred. No. 9e-10;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 CCYDGASVNNDETCEQRAAR 20
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Db      1 CCYDGASVNNDETCEQRAAR 20
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RESULT 6
US-09-878-603-71
; Sequence 71, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czeremak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 71
; LENGTH: 20
; TYPE: PRF
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-71

Query Match
Best Local Similarity 96.5%; Score 110; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 1 CCYDGASVNNDETCEORAR 20

RESULT 7
US-09-878-603-73

Sequence 73, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 73
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-73

Query Match
Best Local Similarity 96.5%; Score 110; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 1 CCYDGASVNNDETCEORAR 20

RESULT 8
US-09-878-603-54

Sequence 54, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-54

Query Match
Best Local Similarity 95.6%; Score 109; DB 9; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAA 19
DB 1 CCYDGASVNNDETCEORAA 19

RESULT 9
US-09-878-603-64

Sequence 64, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-64

Query Match
Best Local Similarity 94.7%; Score 108; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20
DB 1 CCYDGASVNNDETCEORAR 20

RESULT 10
US-09-878-603-65

Sequence 65, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 65
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-65

Query Match
Best Local Similarity 94.7%; Score 108; DB 9; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEORAR 20

Db 1 CCYDGASVNNDETCEQRAAR 20

RESULT 11

US-09-878-603-72
; Sequence 72, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 09/387,671
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-72

Query Match 93.0%; Score 106; DB 9; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.5e-09;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
Db 1 CCYDGASVNNDETCEQRYVR 20

RESULT 12

US-09-878-603-55
; Sequence 55, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czerniak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-55

Query Match 92.1%; Score 105; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRA 18
Db 1 CCYDGASVNNDETCEQRA 18

RESULT 13

US-09-878-603-59
; Sequence 59, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czerniak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 19
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-59

Query Match 92.1%; Score 105; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCYDGASVNNDETCEQRAAR 20
Db 1 CCYDGASVNNDETCEQRAAR 19

RESULT 14

US-09-878-603-66
; Sequence 66, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.
; APPLICANT: Huber-Lang, Markus
; APPLICANT: Sarma, Vidya
; APPLICANT: Czerniak, Boris
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
; FILE REFERENCE: UM-03783
; CURRENT APPLICATION NUMBER: US/09/878,603
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/387,671
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 20
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-66

Query Match 89.5%; Score 102; DB 9; Length 20;
Best Local Similarity 90.0%; Pred. No. 1.3e-08;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCYDGASVNNDETCEQRAAR 20
Db 1 CCYDGASVNNDETCEQRAAR 20

RESULT 15

US-09-878-603-56
; Sequence 56, Application US/09878603
; Patent No. US20020165138A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Peter A.

APPLICANT: Huber-Lang, Markus
APPLICANT: Sarma, Vidya
APPLICANT: Czeizmar, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 17
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-56

Query Match 88.6%; Score 101; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCYDGASVNNDETCQR 17
|||||
Db 1 CCYDGASVNNDETCQR 17

Search completed: May 1, 2003, 22:35:14
Job time : 45 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 1, 2003, 22:24:53 ; Search time 29 Seconds
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Title: US-09-651-685A-5
Perfect score: 114
Sequence: 1 CCYDASVNDPTEQRNAR 20

Scoring table: BLOSUM62
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Searched: 262574 seqs, 29422922 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 08
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	35	30.7	16 1 US-08-137-800-14	Sequence 14, Appl
2	35	30.7	16 1 US-08-477-383-14	Sequence 14, Appl
3	35	30.7	16 1 US-08-487-174-14	Sequence 14, Appl
4	35	30.7	16 1 US-08-480-750-14	Sequence 14, Appl
5	35	30.7	16 1 US-08-441-502B-31	Sequence 31, Appl
6	34.5	30.3	18 1 US-08-137-800-32	Sequence 32, Appl
7	34.5	30.3	18 1 US-08-477-383-32	Sequence 32, Appl
8	34.5	30.3	18 1 US-08-487-174-32	Sequence 32, Appl
9	34.5	30.3	18 1 US-08-480-750-32	Sequence 32, Appl
10	34	29.8	15 4 US-08-975-040-3	Sequence 3, Appl
11	34	29.8	19 1 US-08-392-646-18	Sequence 18, Appl
12	34	29.8	19 4 US-08-975-040-2	Sequence 2, Appl
13	34	29.8	19 4 US-08-975-040-19	Sequence 19, Appl
14	34	29.8	19 4 US-09-101-927-17	Sequence 17, Appl
15	34	29.8	19 4 US-09-101-927-19	Sequence 19, Appl
16	34	29.8	19 4 US-09-441-502B-30	Sequence 30, Appl
17	32	28.1	18 1 US-08-159-340A-32	Sequence 32, Appl
18	31	27.2	16 1 US-08-574-763-3	Sequence 3, Appl
19	31	27.2	20 5 PCT-US95-06726-19	Sequence 19, Appl
20	30	26.3	11 3 US-08-838-413A-14	Sequence 14, Appl
21	29.5	25.9	18 1 US-08-137-800-13	Sequence 13, Appl
22	29.5	25.9	18 1 US-08-137-800-31	Sequence 31, Appl
23	29.5	25.9	18 1 US-08-477-383-13	Sequence 13, Appl
24	29.5	25.9	18 1 US-08-477-383-31	Sequence 31, Appl
25	29.5	25.9	18 1 US-08-487-174-13	Sequence 13, Appl
26	29.5	25.9	18 1 US-08-487-174-31	Sequence 31, Appl
27	29.5	25.9	18 1 US-08-480-750-13	Sequence 13, Appl

28	29.5	25.9	18 1	US-08-480-750-31	Sequence 31, Appl
29	29	25.4	10 1	US-08-421-702A-79	Sequence 79, Appl
30	29	25.4	10 1	US-08-303-052A-32	Sequence 32, Appl
31	29	25.4	10 1	US-08-421-696A-79	Sequence 79, Appl
32	29	25.4	10 1	US-08-421-697A-79	Sequence 79, Appl
33	29	25.4	10 1	US-08-421-698A-79	Sequence 79, Appl
34	29	25.4	10 2	US-08-421-695A-32	Sequence 32, Appl
35	29	25.4	10 3	US-08-461-384B-9	Sequence 9, Appl
36	29	25.4	10 3	US-08-407-207A-6	Sequence 6, Appl
37	29	25.4	13 4	US-09-136-769A-7	Sequence 7, Appl
38	29	25.4	13 4	US-09-136-769A-18	Sequence 18, Appl
39	29	25.4	13 4	US-08-335-303-20	Sequence 20, Appl
40	29	25.4	19 1	US-08-290-448A-49	Sequence 49, Appl
41	29	25.4	19 1	US-08-290-448A-49	Sequence 49, Appl
42	29	25.4	19 1	US-08-175-069A-49	Sequence 49, Appl
43	29	25.4	19 4	US-08-461-939B-49	Sequence 49, Appl
44	29	25.4	19 4	US-08-464-000-49	Sequence 49, Appl
45	29	25.4	19 4	US-08-464-000-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-08-137-800-14
; Sequence 14, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hilliard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Santos, Amelfina D.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137, 800
; FILING DATE: 19-OCT-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-104763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..14
; OTHER INFORMATION: /note= "Xaa(6) is Pro or
; OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro;
; OTHER INFORMATION: Xaa(14) is Asp or beta-carboxyaspartate"

US-08-137-800-14

Query Match

Best Local Similarity 42.9%; Score 35; DB 1; Length 16;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;QY 1 CCYDGASVNDNDEC 14
1 : 1111 1
Db 3 CSHXACSVNNXXIC 16

RESULT 2

US-08-477-383-14
; Sequence 14, Application US/08477383
; Patent No. 5589340
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurflino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,383
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..14
; OTHER INFORMATION: /note= "Xaa(6) is Pro or
; Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp or
; OTHER INFORMATION: beta-carboxyaspartate."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."

US-08-477-383-14

Query Match

Best Local Similarity 42.9%; Score 35; DB 1; Length 16;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;QY 1 CCYDGASVNDNDEC 14
1 : 1111 1
Db 3 CSHXACSVNNXXIC 16

RESULT 3

US-08-487-174-14
; Sequence 14, Application US/08487174
; Patent No. 5595972
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurflino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,174
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..14
; OTHER INFORMATION: /note= "Xaa(6) is Pro or
; Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp
; OTHER INFORMATION: beta-carboxyaspartate."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."

US-08-487-174-14

Query Match 30.7%; Score 35; DB 1; Length 16;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETC 14
| : |||| |
Db 3 CSHXACSVNXXIC 16

RESULT 4

US-08-480-750-14
; Sequence 14, Application US/08480750
; Patent No. 5633347
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurflino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,750
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/137,800
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/084,848
; FILING DATE: 29-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107673
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus bandanus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6..14
; OTHER INFORMATION: /note= "Xaa(6) is Pro or
; OTHER INFORMATION: Hydroxy-Pro; Xaa(13) is Pro or Hydroxy-Pro; Xaa(14) is Asp or
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16
; OTHER INFORMATION: /note= "The C-terminus is
; OTHER INFORMATION: preferably amidated."

US-08-480-750-14

Query Match 30.7%; Score 35; DB 1; Length 16;
Best Local Similarity 42.9%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 1 CCYDGASVNNDETC 14
| : |||| |
Db 3 CSHXACSVNXXIC 16

RESULT 5

US-09-441-502B-31
; Sequence 31, Application US/09441502B
; Patent No. 6455041
; GENERAL INFORMATION:
; APPLICANT: Dundar, Bonita S.
; TITLE OF INVENTION: IMMUNOGENIC EPITOPES OF THE HUMAN ZONA PELLUCIDA PROTEIN
; FILE REFERENCE: 12231.20501
; CURRENT APPLICATION NUMBER: US/09/441,502B
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 31
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-502B-31

Query Match 30.7%; Score 35; DB 4; Length 19;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 CCYDGASVNN 10
| | | | |
Db 5 CCYSSEEVNS 14

RESULT 6

US-08-137-800-32
; Sequence 32, Application US/08137800
; Patent No. 5514774
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Hillyard, David R.
; APPLICANT: Macintosh, J. Michael
; APPLICANT: Santos, Ameurflino S.
; TITLE OF INVENTION: Conotoxin Peptides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,800
; FILING DATE: 19-OCT-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-104763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3..4
OTHER INFORMATION: /note="Xaa is Pro or Hydroxy-Pro"
US-08-137-800-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY 1 CCYDGA-SVNDETC 14
||:|:||||:|
Db 4 CCSPACVNNPQIC 18

RESULT 7
US-08-477-383-32
Sequence 32, Application US/08477383
Patent No. 5589340
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurifino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,383
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Imnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORGANISM: Conus ermineus

ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note="Xaa is Pro or Hydroxy-Pro."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /note="The C-terminus is preferably amidated."
US-08-477-383-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY 1 CCYDGA-SVNDETC 14
||:|:||||:|
Db 4 CCSPACVNNPQIC 18

RESULT 8
US-08-487-174-32
Sequence 32, Application US/08487174
Patent No. 5593972
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Ameurifino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,174
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Imnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus

FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /note="Xaa is Pro or Hydroxy-Pro."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /note="The C-terminus is
OTHER INFORMATION: preferably amidated."
US-08-487-174-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 CCYDGA-SVNNDETC 14
DB 4 CCSNPACVNNPOIC 18

RESULT 9
US-08-480-750-32
Sequence 32, Application US/08480750
Patent No. 5633347
GENERAL INFORMATION:
APPLICANT: Olivera, Baldomero M.
APPLICANT: Cruz, Lourdes J.
APPLICANT: Hillyard, David R.
APPLICANT: Macintosh, J. Michael
APPLICANT: Santos, Amelino S.
TITLE OF INVENTION: Conotoxin Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,750
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/137,800
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,848
FILING DATE: 29-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24260-107673
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Conus ermineus
FEATURE:
NAME/KEY: Modified-site

LOCATION: 3
OTHER INFORMATION: /note="Xaa is Pro or Hydroxy-Pro."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: /note="The C-terminus is
OTHER INFORMATION: preferably amidated."
US-08-480-750-32

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 46.7%; Pred. No. 35;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 CCYDGA-SVNNDETC 14
DB 4 CCSNPACVNNPOIC 18

RESULT 10
US-08-975-040-3
Sequence 3, Application US/08975040
Patent No. 6251620
GENERAL INFORMATION:
APPLICANT: HATADA, MARCOS
APPLICANT: LU, XIABO
APPLICANT: LAIRD, ELLEN
APPLICANT: KARAS, JENNIFER
APPLICANT: ZOLLER, MARK
APPLICANT: HOLT, DENNIS
TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING
TITLE OF INVENTION: TO ZAP-FAMILY PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID L. BERSTEIN, ARIAD PHARMACEUTICALS,
STREET: 26 LANDSDOWNE STREET
CITY: CAMBRIDGE
STATE: MA
COUNTRY: US
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,040
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/605,578
FILING DATE: 22-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, DAVID L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 347F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-1828
TELEFAX: 617-494-1828
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product="phosphotyrosine"
OTHER INFORMATION: /label="pTyr
OTHER INFORMATION: /note="phosphorylated tyrosine"

NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: /product="phosphotyrosine"
OTHER INFORMATION: /label= ptyr
OTHER INFORMATION: /note="phosphorylated tyrosine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product="Acetylated"
OTHER INFORMATION: /label= Ac
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: /product="amidated"
OTHER INFORMATION: /label= NH2
US-08-975-040-3

Query Match 29.8%; Score 34; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 YDGASVNDCTE 15
| | | | |
Db 1 YTGSLSTRNOETYE 13

RESULT 11
US-08-392-646-18
Sequence 18, Application US/08392646
Patent No. 5710129
GENERAL INFORMATION:
APPLICANT: LYNCH, Berkley A.
APPLICANT: WEIGELE, Manfred
TITLE OF INVENTION: NEW INHIBITORS OF SH2-MEDIATED PROCESSES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Pharmaceuticals, Inc.
STREET: 26 Landsdowne Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139-4234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,646
FILING DATE: 23-FEB-1995
CLASSIFICATION: 560
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 337
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product="phosphotyrosine"
OTHER INFORMATION: /label= YPO4
OTHER INFORMATION: /note="phosphorylated tyrosine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15

NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: /product="phosphotyrosine"
OTHER INFORMATION: /label= YPO4
OTHER INFORMATION: /note="phosphorylated tyrosine"
US-08-392-646-18

Query Match 29.8%; Score 34; DB 1; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 YDGASVNDCTE 15
| | | | |
Db 4 YTGSLSTRNOETYE 16

RESULT 12
US-08-975-040-2
Sequence 2, Application US/08975040
Patent No. 6251620
GENERAL INFORMATION:
APPLICANT: HATADA, MARCOS
APPLICANT: LU, XIADDE
APPLICANT: LAIRD, ELLEN
APPLICANT: KARAS, JENNIFER
APPLICANT: ZOLLER, MARK
APPLICANT: HOLT, DENNIS
TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING
TO ZAP-FAMILY PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID L. BERSTEIN, ARIAD PHARMACEUTICALS,
INC.
STREET: 26 LANDSDOWNE STREET
CITY: CAMBRIDGE
STATE: MA
COUNTRY: US
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,040
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/605,578
FILING DATE: 22-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, DAVID L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 347F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-1828
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product="phosphotyrosine"
OTHER INFORMATION: /label= ptyr
OTHER INFORMATION: /note="phosphorylated tyrosine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15

OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= ptyr
OTHER INFORMATION: /note= "phosphorylated tyrosine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "acetylated"
OTHER INFORMATION: /label= Ac
FEATURE:
NAME/KEY: Modified-site
LOCATION: 19
OTHER INFORMATION: /product= "amidated"
OTHER INFORMATION: /label= NH2
US-08-975-040-2

Query Match 29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 YDGASVNDCE 15
DB 4 YTGSTRNOEY 16

RESULT 13
US-08-975-040-19
Sequence 19, Application US/08975040
Patent No. 6251620
GENERAL INFORMATION:
APPLICANT: HATADA, MARCOS
APPLICANT: LU, XIODE
APPLICANT: LAIRD, ELLEN
APPLICANT: KARRS, JENNIFER
APPLICANT: ZOLLER, MARK
APPLICANT: HOLT, DENNIS
TITLE OF INVENTION: MACHINE READABLE STORAGE MEDIUM RELATING
NUMBER OF INVENTION: TO ZAP-FAMILY PROTEINS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID L. BERSSTEIN, ARIAD PHARMACEUTICALS,
STREET: 26 LANDSDOWNE STREET
CITY: CAMBRIDGE
STATE: MA
COUNTRY: US
ZIP: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975.040
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/605.578
FILING DATE: 22-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BERSSTEIN, DAVID L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 347F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-1828
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= YPO4
OTHER INFORMATION: /note= "phosphorylated tyrosine"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: /product= "phosphotyrosine"
OTHER INFORMATION: /label= YPO4
OTHER INFORMATION: /note= "phosphorylated tyrosine"
US-08-975-040-19

Query Match 29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 YDGASVNDCE 15
DB 4 YTGSTRNOEY 16

RESULT 14
US-09-101-927-17
Sequence 17, Application US/09101927
Patent No. 6303319
GENERAL INFORMATION:
APPLICANT: RICKLES, Richard J
TITLE OF INVENTION: Cell-Based Assay
FILE REFERENCE: 336A PCT/US
CURRENT APPLICATION NUMBER: US/09/101.927
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: PCT/US97/026735
EARLIER FILING DATE: 1997-02-21
EARLIER APPLICATION NUMBER: 60/012,218
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 17
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: PHOSPHORYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (15)
OTHER INFORMATION: PHOSPHORYLATION
US-09-101-927-17

Query Match 29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 3 YDGASVNDCE 15
DB 4 YTGSTRNOEY 16

RESULT 15
US-09-101-927-19
Sequence 19, Application US/09101927
Patent No. 6303319
GENERAL INFORMATION:
APPLICANT: RICKLES, Richard J
TITLE OF INVENTION: Cell-Based Assay
FILE REFERENCE: 336A PCT/US
CURRENT APPLICATION NUMBER: US/09/101.927
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: PCT/US97/026735

; EARLIER FILING DATE: 1997-02-21
; EARLIER APPLICATION NUMBER: 60/012,218
; EARLIER FILING DATE: 1996-02-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: PHOSPHORYLATION
US-09-101-927-19

Query Match 29.8%; Score 34; DB 4; Length 19;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 YDGASVNNDETC 15
| | | | |
Db 4 YTGILSTRNOETVE 16

Search completed: May 1, 2003, 22:28:15
Job time : 30 secs